

FIGURE 1

CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGACAGTGAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACCTCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTC
CTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG
CTGGACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCCCTGGTTACCCCAACGGCATCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAA
CGTGAAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGT
TACAAAT

1304.F001

FIGURE 2

MTDSPPPGHPPEEKATPPGGTGHEGLSGGAADVASGVSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FOOTNOTES

FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
GTCAGCCACGCGCGGGGACTATGGTGAAATTCGCGGCGCTCACGCACTACTGGCCCCCTGATC
CGGTTCTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGTTT
GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCTGTGTATGGTGGTGGCAGGGGCCATCGC
TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT
CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAAACACAAATACAGTTT
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC
TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC
GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTACGACATCATCCC
TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT
CTCACCGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGCCCCAGCTCTGTGCTGCG
GATCATCGTCTCATCGCCAGCCTCGTGGTCTACCTACCTGGGGGTGCACGGTGCAGCCC
TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTGCATCGCTGCG
TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGAAATGAGAGAGG
AGAATGAATAAGGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTGTGTTTGTGTTTGGTAAT
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC
TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC
TCCTCCCTGGACAATCTCCTCTTGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT
CACCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG
TTAAAACTCGGCTTCCTTTGATTTGCTTCCCAGTCACATGGCCGTACAAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
GAGGCGGGTGGCAGCTGCAGCCCGGAGTCCCCGTTCACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG
GGCAGCAAACCTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA
GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTACAAAA
GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC
CTTTCCTGAAGGTCGATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT
TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTTCTAATGCCAGGTTGCTGTAGGGTAA
TTTTGAAGTAGATATATTACCTGGTCTGTCTATCCTTAGTCATAACTCTGCGGTACAGGTAA
TTGAGAATGTACTACGGTACTTCCCTCCCACACCATAACGATAAAGCAAGACATTTTATAACG
ATACCAGAGTCACTATGTGGTCTCCTCGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA
TATTTTCTAAGTTTTGGAAGCAGGTTTTTTTCTTTAAAAAAATTATAGACACGGTTCACT
AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATTTTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTATTTTCGC
ATTTTCAATAAAATGTCTCTAATACAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSDFKNVGLVFNNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYIINKLHHVDESV
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSTNTVTAHHKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGvHGATLGvGSLL
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPPTEEVTDIVEMRENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

FOOTNOTES

[illegible][illegible]

FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTTCCTTTGCGGATTTTCT
CCTTTTTCCAGTTCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG
AAACCTTTGTCCTTGCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

FOOT = 100.000

FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

FIGURE 7

FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCAGTTCTTCCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT
TCTTTTTACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT
CTACTTGCTGTGCATCGCGGCCGTGGCGCTGATGTTTCATGTACTACTGAGCCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTCTGCCAAGGTCCAGGACGCCAGCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT
GGCCTCACTGCACGTCTATGATGACGCTACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCTTCCCCTCCTCCCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT
CCTGGTCAGTCCCCCAGGGGACCCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAACAAGCCAGTGCGTGTAACAAAAA

FOH201-1302FOF

FIGURE 9

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLLFTFFLFLGVLSIIMLSPGVE
SOLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW
NQRWLKGAEEDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVA
ACEGRAFDNEQDGVITYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS
WAGLLLLYLWTLVAPLLLLNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

TOC-1000

FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCGAGTCTTTGCTGCCGAAGCTG
TGA CTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCTGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA
GCTGTACCGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACCTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCTTAGAAACC
CTTCAGTAATAGATAAAACAAGACAAGGACTGAAAGTGCTCTGAACTTGAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTTCTTTCTT
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTTCGAAAAGATTAAAGTTGAATTTTACAGTTT

FIGURE 10

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDAVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRQLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FOOTNOTES

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAAGACGGGCTTCCCTACGTCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGCGAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG
GCTGGCGCCGAACC

[illegible]

FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

FOOTNOT 430/FOOT

[illegible]

FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

TDI207-1802007

FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

TOP OF FOOT

FIGURE 17

AATCCCAAATTCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

FOOTNOTES

FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

FOOTNOTES

FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCTTCCACCTGATTGTGTCTATGACTGGCTG
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCCG
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAGAGCAGGGGGCTCTCCTCAGAAAT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAC'TGCTCCTGA
GGAGGCCCCCTGGGCCTCTGCCTCEGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACT
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGTCTGTCACATATGCATAAGTA
CTTTTACAAGTTGTCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGAGACATTTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCCAACGAAAAATAATCTGGCCCAAATGTGAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCCAGCCTCATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCACAAAAACAGCTGTCGCCAAACACCG
ACTCTGTCGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATCTGG
TTGTTTGTAGCCTAA

FIGURE 19

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAPVFEGLLVLRCAWQDWPLTQVTFFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSAAPTILNPAPQKSAAPGTAPPEAPGPLPPPPTPSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

1001084-102400

FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTACCTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC
TGGCAGCGGTTATGGCTTCACGGTGGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCTTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGAGGCTTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTGTTAAAAATGCCCCATTAGGC
CAGGATCTGCTGACATAATTGCCTAGTCAGTCTTGCCTTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTTCCCTGGATAGCCCAAAGTGTCCGCTACCAACACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

FIGURE 21

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPCYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSYHTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAILLIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

FIGURE 22

THE

NEW YORK PUBLIC LIBRARY

ASTOR LENOX TILDEN FOUNDATION

1900

NEW YORK

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

amino acids 232-251

FIGURE 25

FIGURE 25

GTCGTTCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCTCAGCCGCTGTGCGAGGAGAGCACC CGGA
 GACGCGGGCTGCAGTCGCGCGGCTTCTCCCGGCTGGGCGGCTCGCCGCTGGGCGAGGTGCTGAGCGCCCTAG
 AGCCTCCCTTGCCGCTCCCTCCTCTGCCCCGCGCAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCG
 GCCCCGGAGGCGCGGTGGATGCGGCGCTGGGCGAAGCAGCCGCCGATTCCAGCTGCCCGCGCGCCCCGGGCG
 CCCCTGCGAGTCCCCGGTTAGCCATGGGGACCTCTCCGAGCAGCAGCACC GCCCTCGCCTCCTGCAGCCGCATC
 GCCCCCGGAGCCACAGCCACGATGATCGCGGCTCCCTTCTCCTGCTTGGATTCCCTAGCACCACCACAGCTCAG
 CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
 GACAAGTGTCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
 GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG
 ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCATTGCCACCTGGCATGTTCCAGTCTAACGCT
 ACCTGTGCCCCCATACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
 TGTAAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
 CTGAGTCAGAACCTGGTGGTGTATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTTCT
 TCCAGCTCCACCTCACCTTCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT
 TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACTCTTCTGCCTCTGTTAGACCAAAGGTACTG
 AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
 CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
 GCCACTGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
 CATTGTGACATCAATGAGCATTGCCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGCTTGTGGTGATTGTGGTG
 TGCAGTATCCGGAAGCTCGAGGACTCTGAAAAAGGGGCCCGGCAGGATCCCAAGTCCATTGTGGAAAAGGCA
 GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
 ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
 AGGGAGGTGTGCTGCTTTCTCAATGGGTACACAGCCGACCAGAGCGGGCCTACGCAGCTCTGCAGCACTGGACC
 ATCCGGGGCCCCGAGGCCAGCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCCGAGAAACGATGTTGTGGAG
 AAGATTCTGTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAAACTAGCTCTCCCGATGAGCCCCAGCCCG
 CTTAGCCCCGAGCCCCATCCCCAGCCCCAACCGGAAACTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA
 CAGGACAAGAACAAAGGGCTTCTTGTGGATGAGTGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
 TCCGCGCTGAGCAGGAACGTTCTTTTATTAACAAAGAAAAGAGACACAGTGTGCGGCAGGTACGCCTGGAC
 CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTATTGAAGAG
 ATTCCCAGGCTGAGGACAACTAGACCGGCTATTGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
 CTCCTGACTCTGTTTATAGCCATCTTCTGACCTGTGTAGAACATAGGGATAGTGCATTCTGGAAATTACTCA
 ATTTAGTGGCAGGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTTTGT
 GT
 TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA
 ATACCCACCACTAAAGTTTTTTAAGTTCCATATTTCTCCATTTTGCCTTCTTATGTATTTTCAAGATTATTCTG
 TGCATTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
 TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT
 AAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTCTTAAAGATTAAAGAAATTTAAGA
 CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTAAATATGTCTTGTATAGTTCAATTCATGG
 CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTCACTGGACACCGTGTAGAATGCTTGATTACTTGTAC
 TCTTCTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTGCTATTTAAGTGGCTT
 GACAACTGGGCCACCAAAGAACTTGAACCTTCACTTTTAGGATTGAGCTGTTCTGGAACACATTGCTGCATTT
 GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
 TTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCCTTGGTCTGGTGGGATTCTTCAACCAATT
 ACTTTAATTAATAATGGCTGCAACTGTAAGAACCTTGTCTGATATATTTGCAACTATGCTCCATTTACAAATG
 TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAGGTGGCGTGGACTCCCTTGTGTGGGTGGGGTTTGTGG
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTA
 AAAAAAAA

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLPCA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWVRKKGTTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMTPTONREKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRG
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLEDVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 26

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCC
TTGATGATTTGAAAATAAGTCTGTTCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAAC
TGGGTTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGAGTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCCTTGCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTCTATCAC
GCCCCGTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAAGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCTGTCTGAACCACGCGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
CCGTGTACCTCCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCGGGCACCA
GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCAGCACAACCTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTTGGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAATAATTTTGTATTTTAGTAGAGAC
AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC
TGATCTTCACTAAGAACAAGAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC
ACTGCACGTTTTTCATCTCTAGGGACCAGAACCAACCCACCCTTCTACTTCCAAGACTTAT
TTTACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT
TGTAGCATTTGGTGCTTGACGTATTATTGTCCTTTGATTCAAATAATATGTTTCCTTCCT
CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVFTAAS
WKTMCSDDWKGYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVLTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIIITAAHCYVDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGVKVCWTSWGATEDGGDASPVLNHAAPVPLISNKICNHR
DVGGLIISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSFQIGCAEVNKPQVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

FIGURE 28

FIGURE 29

CCCACGCGTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGTCTATTTATTGCAACGGTCAAGGCTGGCTTGT
 GCCAGAACGGCGCGCGCGCGCACGCACGACACACGGGGGAAACTTTTTTAAAAATGAAAGGCTAGAAGA
 GCTCAGCGCGCGCGCGCGCGCTGCGCGAGGGTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCCGCA
 CGCCCGCGCGCGCTCGGCGCCGCGTGGGATGGTGCAGCGCTCGCCGCGGGCCGAGAGCTGCTGCACTGAAG
 GCCGGCGACGATGGCAGCGCGCGCGTGGCGTGTCCCCGCGCGCCCTCCTGCTCGCCCTGGCCGGTGTCT
 GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCTAGTGCCTCTGT
 TCGGAGTGGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTCTGACT
 ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC
 CCCTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT
 ACGGGGATATTCTGATTCTAGCAGTCACTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTGAAAATGA
 AAGCTATGTCTTAGAACCAATGAAAAGTGAACCAACAGATACAACTCTTCCAGCGAAGAAGCTGAAAAGCGT
 CCGGGGATCATGTGGATCACATCACACACCAAACTCGTGCAGAAAGATGTGTTCCACCACCTCTCAGAC
 ATGGGCAAGAGGCATAAAAGAGAGACCTCAAGGCAACTAAGTATGTGGAGCTGGTGTGCTGGCAGACAACCG
 AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAGGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAA
 GTTTTACAGACCACTGAACATTTCGGATCGTGTGGTAGGCGTGAAGTGTGGAATGACATGGACAAATGCTCTGT
 AAGTCAGGACCCATTCCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAAATCCCA
 TGACAAATGCGCAGCTTGTCTAGTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG
 CACGGCAGACCACTCTGGGGGAATTGTCTAGTGACCATTCAGACAATCCCCCTTGGTGCAGCCGTGACCTGGCACA
 TGAGCTGGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACCGGTTACCCATTTCCATGGTGTTCAGCAGTGTGACAGGAAGGACTT
 GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCGGGAAGTCAGGGAGCTTTTCGGGGGCCA
 GAAGTGTGGGAACAGATTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
 CTGCAATGCCACCACCTGTACCCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
 GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC
 TCACTGCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
 CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
 GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCTTTGCCAAATGCGAGAT
 GAGAGATGCTAAATGTGGAAGAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTATTGGTACCAATGCCGTTTC
 CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTACTTTGGGCGATGA
 CATGCCGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
 AAATATTAGTGTCTTTGGGGTTTACGAGTGTGCAATGCAGTGCACCGGAGAGGGGTGTGCAACACAGGAAGAA
 CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTTGAGGAAGCACAGACAGCGGCC
 CATCCGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGCCAGGGCCAGGAGCCCGTGGG
 ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCAGTG
 CTGCTGCAGAGGAGGTCAAGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
 TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
 CAGTGCAGGAAGGGCAGCGACTTCTGTTGAGCTTCTGCTAAAAACATGGACATGCTTCAGTGTGCTCCTGAG
 AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTT
 ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCTTTCCCAAGTGACACCTCAGCCT
 TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTATTATATGAAAAAT
 AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATCTCCATCCAAGCAAAGTGAATGGCAA
 TGAAACAAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACCTGGCTCTTTGCTGTGGACATGCGTGACCAGC
 AGTACTCAGGTTTTGAGGTTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCCTTCAATTAACAAGTAAGAA
 TGTAAAAAGTGAAAAAATGTAAGAGCCTAACTCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
 GAAAT

FIGURE 29

FIGURE 30

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
```

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWI PVKS FDSK
NHPEVLNIRLQRESKELI INLERNEGLIASSFTTETHYLQDGT DVSLARNYTGHCYYHGHV RG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQ GKDLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKL LPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNF GMNHD TLDRGCSQMAVEK
GGCIMNASTGYPPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNR FVEEGEE

CDCGEPEECMNRCCNATTCTLKPD AVCAHGLCCEDCQLKPAGTACRDS SNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN
CGKVS KSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLN RQCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGP I RQAEARQEAAESNRERGGQGE PVGSGEHA STASLTLI

Signal peptide:

amino acids 1-28

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCAGTGTCCTTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

FIGURE 31

FIGURE 32

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTTGGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACCCCGCCACAACTTTTTAAGAAGTTAAT
GAAACCATACCTTTTACATTTTAAATGACAGGAAAATGCTCACATAATTGTAAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA
TACCAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAACAAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGAAAAATCACGCCACTTGGGAAAAAAGATTGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGGTAAGGGGATGGTGGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT
CCTTTAACAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL

LHLYH

Signal peptide:

amino acids 15-27

FOOT - HEAD FOOT

FIGURE 34

CCCGCGGCGAGAGCGCGCCAGCCCCGCGCGATGCCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC
 CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCGGGCCAGG
 AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCGAGCGGCGAGGACGGACAGGACCCCGCACAGCAAGCACC
 TGTACACGGCCGACATGTTTACGCACGGGATCCAGAGCGCCGCGCACTTCGTTCATGTTCTTCGCGCCCTGGTGTG
 GACACTGCCAGCGGCTGCAGCCGACTTGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
 ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGGCAGGATACCCACCTTAA
 AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCTCGGGACTTCCAGACACTGGAAAACCTGGATGC
 TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGGAAACCGCCAGTGCCCCGAGCTCAAGCAAG
 GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC
 CGTGGTGTGGTCACTGCAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCTTGAACATTCCGAAACTG
 TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGAAACCAGGTTCTGGCTATCCCACTC
 TTCTCTGGTTCCGAGATGGGAAAAGGTGGATCAGTACAAGGAAAGCGGGATTGGAGTCACTGAGGGAGTACG
 TGGAGTCGAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCGGTGCTGGCAG
 CTGAGCCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAA
 TAACCTTTCATCAAGTTTATGCTCCATGGTGTGGTCACTTGTAAAGACTCTGGCTCCTACTTGGAGGAACTCTCTA
 AAAAGGAATTCCTGGTCTGGCGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
 AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCGAGGAGGAAGAAAGTCAGTGAGCACAGTGGAGGCA
 GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGCAAGCACTTTAGGAACACAGTTGAGGTCAC
 CTCTCTGCCAGCTCCCGCACCTGCGTTTAGGAGTTTCACTCCACAGAGGCCACTGGGTTCCCACTGGTGGCT
 GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTCTTTGTGTGTGTGTTTCCAAGCCAACACACTCTACAG
 ATTCTTTTATTAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCACTGGTCACTGTGTAAACATTTTCACTGGCGATA
 TATCCCCCTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA
 TTGCTGGACTATTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCAAAGCATAGTTTACCTGC
 CCACGAGTTCTGAAAGGTGGCCTTGTGGCAGTATTGACGTTTCTCTGATCTTAAGGTCAAGTTGACTCAATAC
 TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACTCTGGAAGATACCTTCACGGCCGCTGC
 TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
 GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTGATACTTGTCAAATCAGTTACTGTTCAAGGGAT
 CCTTCTGTTTCTCACGGGTGAAACATGTCTTTAGTTTCTCATGTTAACACGAAGCCAGAGCCACATGAACTGT
 TGGATGTCTTCTTAGAAAGGGTAGGCATGGAATAATCCACGAGGCTCATTCTCAGTATCTCATTAACTCATTGA
 AAGATTCCAGTTGTATTTGTCACTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCTGGGTATCCAGGGAGGC
 TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG
 CTTGTCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC
 CAAAGACAGATGTGAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
 ACTCATGCTGTCCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
 GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCATAATAACCACTTTGCATCCAACACTTTCACCCACCT
 CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA
 TGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTTGCCTTAAAGGAAATCTTTATTAATCAG
 TATGGTTTACAGATAATTCTTTTAAAAAAACCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTGATA
 CACAACCTCAGCTTTGCATCAGAGTCTTGTATTCCAAGAAATCAAAGTGGTACAATTTGTTTGTACTAT
 GATACTTTCTAAATAAACTCTTTTTTTTTAA

E01201-130000

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRYPTLKLFPKGQEA VKYQGPRDFQTLNWM LQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASN FELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QH YELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLES LREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFD D TIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDLH R FVLSQAKDEL

Signal sequence:

amino acids 1-32

FIGURE 35

FIGURE 36

CTTTTCTGAGGAACACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCCG
GGTGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTCAATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACCTTCCCTCATCCT
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAAAAA

FIGURE 36

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEGEEG
KHGKVGRMGPKGIKGEIGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY
RKFFVGQLDISIARLKTSMKFVKNVIAGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

FOOTNOTES

FIGURE 38

GGTTCTATCGATTCTGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCCCGTGTGGAGTGGTGGGGCCCTGGGTGGGAATGGGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCCAGCAGCGCGCCGCGC
ACACCTTTCTCATTACAGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGCGGACAG
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT
CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG
GTTCCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCCGCCCTGCGCCGGGGCC
CCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG
GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG
CCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC
ACCTCTGGCACCACGGGCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC
TCTACCACATGTCCGGTTCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAG
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT
TTTGTGCGGCGCTTCGGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
GGCCACCATCAACTACACAGGACAGCGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC
ATATCTTCCCCCTTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAATTCCGGACCCC
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA
GCAGTCCCCATTCTGGGCTATGTGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG
ATGTCTTCCGGCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCCCTACCTGCCCCCTCACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA
CCTTCGAATCTGAGAACTTCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG
CCGTTGCAGGTGTACTGGGCTGTGAGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAGGGCGGCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

FIGURE 38

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTAPWKEKSQLERAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL
LLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRRFSYSEAESNRARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVRRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGORGAVGRASW
LYKHIFPFSRLIRYDVTTGEPIRDPOGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGK
LLKDVFRPGDVFFNTGDLLVCDDQGFRLRFHVRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

[illegible]

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTELKRYT TGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKI SEAIMNMQENSMQVS AKVFQGCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDES VTAGTSNEEECWNGH SKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

protein: 430C.F001

FIGURE 42A

GenBank: F00440

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCCGCTGGTGAGTGTGCGGGAGATTGGCAAACGCCTAGG
AAAGGACTGGGAAAATAGCCCTGGGAAAGTGAGAAAGTGATCAGGAGGCCGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA
TCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTGAGGGCGCTCTGGCCACGA
AAAGTTCCTGTCCACTGTGATTCTCAATTCCTTGCTTGGTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATAATTA
ACTTTTTTCTTTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATCCATTAAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCCTGTGTTGGGTGCATG
TGTGCGCCCGCAGCGGCGCGGGGCGGTGGTTCTCCGCTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
GGGCTGTGCGGGCATCCGCCTCCGCCTTCTCCACAGGCCTGTGTCTGTCTGCTGGAAGATGCTAGCAATGGGG
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGCGGGCCAGGCCTTAGAAGAGGAGG
AAGAAGGGGCCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACTTCCACCTCCAGCCCCATCTCA
TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTACCACGGATCTGAGATTAAAAACCTACTCTTG
ACAAGCTCGCTGCCGAAGGAGTTAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT
TTATTACTGGAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCACTGTTTAC
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAATGGCACT
TGGGTTTTTAACAGAAAAGAATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG
GGGATTACTATACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA
ACCCCAAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTTCACTTACCAGTCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCTGCTTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGATAACATTGACCCCTATACACCAAGGC
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGATGGCTTTTCAACATCAGCCGACCCATATGA
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCAGATTCAACAAAAC
TGCAGTGCCGGTCAGGTATCCCCCAAGACCCAGAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAAGAGGAAACCAAGAAAAGAAGCCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAA
GAAGAAGAAAACAGCAGAAAGCAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
GGCTTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAAGTGTCTGCTCAGTG
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG
GTGAGTCTTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAACACTGCTTTGAATTATAGGAGGAGAACATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGAGTGCATGATTAAACTACCTTTGATAAATTAC

FIGURE 42B

AGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTGCATATGA
CACTTGGGTTTTTTAATTAATTCTATTTTATATATATAAATATATGTTTCTTTTCCTGTGAAAAGCTGTTTTCT
CACATGTGAACAGCTTGCACCTCATTTTACCATGCCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC
ACAATGAATGTAACATTTTTCTAAACACTTTACTAGAAGAACATTTTCACTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTGTTGTTTTTATAAAAAGTTATGCAAATGACTTTTATTTTTATTTCTGCATACCATTAGAAGA
ATTTTATTTTCATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAACATCATTTCAGAAAACTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAATTCATGTTTGTGCAGAGTTGAGACAACCTTTATGTTTCTATCATAACTATTTATGTATCTT
AATTATTAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAATT
GTATCATTGGTCCTAAAAAATAAAAATCTTTACTAATAGGCAATGAAGGAATGGTTTGCTAACAACCACAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCATAATAATAACTAA
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCATTAAAAGTAATAACCTTACTCTTATACAAAGT
GGCACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAACCCC
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA
GATTGGTGTGGATCCTGTAGACCTGGTGTCTTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT
CTAGTACTGAAATTACTAAATTTGGGTAAGATGATTTAAATGATTTTAAATTTAACATTTTATTTCTAGAATATAT
GGCTCCATTTTATTTTATAGTGTAAGTTGTATTTCTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 42B

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVG YHGSEIKTPTLDKLA AEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTH MVGKWHLGFN RKEC
MPTRRGFD TFFGSL LGSGDY YTHYKCDSPG MCGYDLYENDNA AWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAML SCLDEAINNVTLA
LKTYGFYNN SIIIIYSSDN GGOPTAGGSNWPLRGSKGTYWEGGIRAVG FVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPROKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FOH20T-1804T00T

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTGTTAGCATCGGCACGTGAGCCT
GGGGTCTGTCACTATGGAATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT
GCAGATGCTTTCCAGGATACACCGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAATCTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAATGTGACA
TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAAATTAATAATGTTACCCACAGAACCCACAGGACTCC
TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAT
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCACAAGAAAGACATTGGCCGATTGAAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCGAGTGTTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGACAAAG
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTGAGTTGTATCAAGGAACTGATGC
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTGAGTTCCCTGGTTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAACTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG
TAAGATGCCTTTCTTGATATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCTTTGTAATAATAA

FIGURE 44

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPKNKRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKLLAHKNSMKKKAKIKNVTPEPTRTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

protein = headfoot

[illegible]

GGGAGCTGTGCTGTGGCTGTGGTGTGCTGTGCGCGCTGCTCCTGCTCTTGGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC
ATGGATAACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVVWTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLEGNLKEKDILVLPLDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQSRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

Photo: headfoot

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
 GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG
 TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC
 TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT
 TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
 GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
 ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
 GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCCC
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
 CTGGGTCTCTCACTGCTGCCCACCTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT
 CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
 GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
 GCAGCTCGCCCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCCGCCATCGCTTCC
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC
 CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACCTGTATCTACAACCAGCT
 GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGGCCCCCAGCCTG
 GGGTGCAGGGCCCCCTGTGAGGAGATTCCGGGGGGCCTGTGCTGTGCCTCGAGCCTGACGGA
 CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
 GCTGCTGACCAACACAGCTGCTCACAGTTCTCTGGCTGCAGGCTCGAGTTTCAGGGGGCAGCTT
 TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
 TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGGCCCTGGGAGGCCAGGCT
 GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG
 CTGCCCCTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA
 CCGGAGGAGTGGGGCCTGAAGCAGCTCATCTGCATGGAGCCTACACCCACCCCTGAGGGGGG
 CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
 TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCGGACGG
 GCCCCCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG
 GGCTGACAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
 TGTGTACCAAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCACTGGTG
 CATGAGGTGAGGGGCACATGGTTCTTGCCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
 CCCCCCAGGCCCGGCGGTCTTACCAGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG
 ACTGGCAGGTCTACTTCGCCCAGGAACCAGAGCCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
 AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
 AGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCTGTCATGTGTGATTCCAGGCAC
 CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA
 CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAGC
 AGGCGTCTCAGCTTTCCTCCTCTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT
 TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTTAACTTAAATAAATTGTTAC
 AAAATAAAA

1002407-1502407

FIGURE 49

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571
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MLLSSLSVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRLNRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYDPDHLDPDGERG
WVLGRARPGAGISSLQTVPVTLTGPRACSRHLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPE
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

[illegible]

FIGURE 50

CGGGCCGCCCCCGCCCCCATTCGGGCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGGGCAGGGGCAGCCTTCCACCACGGGGAG
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCTGCGTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTTCGGCAGCGCTGCCGTGAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT
TGGCAGGATGGGCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCACAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTACCATCACAGGG
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCCAGTGCTGCGTGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTACCCCGGCCTTGTTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC
CCCTCCTTCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCACCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCTGCTGGC
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAAGCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAAA

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGGQVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVNPNVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGELEGSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

TDI001-4804T001

FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGCTGCTTTTTGTAGGGACTTCTTTCTTGCTTCAGCAACATGAGGCTTTTCT
TGTGGAACGCGGTCTTGACTCTGTTCTGTCACCTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCCATTGTTTACCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCTCCTGC
TCTGGGCTATGGAAGAAGGAAAAGGTAATAATCCCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGCAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAACCTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCCTTTTAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTTATACAATGTTCTTTCTTGCTTTGTTTTTTTATTTTTATATATTTTTT
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCTATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCTGTAATCCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCGGAGGTTGCGGTAAGCCGAG
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTCCCATTTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

404201-1802.F001

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL
FHSTHKHNNQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDDKDGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FOOTNOTES

FIGURE 54

[illegible]

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

FIGURE 55

FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCCCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACCTGCTACATCATGAACCCCCC

FOOTNOTES

FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCCCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

101207-18021001

FIGURE 58

TGCGGCGACCGTCGTACACCATGGGCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT
TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGACGTCACCCCCAGTGGTGCTGGTCC
CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA
CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAACCTGCTGCTGCCTGTCATCATTGACTGCTGGATTGACAATA
TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG
GGAAGACCTTCTCACTGGAGTTCTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA
GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG
AAAACGGGCCCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTTGGTGC
TGGTTGCCACAGTATGGGCAACATGTACACGCTTACTTTCTGCAGCGGCAGCCGAGGCTGGAAGGACAAGT
ATATCCGGGCCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAAGACCCTGCGCCTCCTGGCTTCAGGAG
ACAACAACCGGATCCCAGTCACTGGGCCCTGAAGATCCGGGAGCAGCAGCGGTGAGTGTCTCCACCAGCTGGC
TGCTGCCCCTACAACCTACACATGGTCACTGAGAAGTGTTCGTGCAGACACCCACAATCACTACACACTGCGGG
ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG
AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT
ATGAGAGCTTCCCTGACCGTGACCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTTGAAGAGTGGCC
TGCAGTGCCAGGCTGGCAGAGCCGCCAGGAGCACCAAGTGTGTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCG
AGATGCTGGCCAACGCCACCACCTGGCCTATCTGAAACGTGTGCTCCTTGGGCCCCTGACTCCTGTGCCACAGGA
CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCTCTGGGGCTGTATGGCCACGCGTTTTGCAAAAGTTTGTGA
CTCACCATTCAAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCCTTTCTCT
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGA
ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCCAGTCCCTGCCTGGGGCCATG
TGTCCCCCTATTCTGTGGGCTTTTCATACTTGCCCTACTGGGCCCTGGCCCCGAGCCTTCCTATGAGGGATGTT
ACTGGGCTGTGGTCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCTTCCCACACACCA
GCCACAGATAGGCCTGCCACTGGTCACTGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC
TGACTGGCTTCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTGTGCGTTCTTCGTGGTTCCCAGGC
CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG
CCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC
CTCCCTTACCCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTGGAGCCATGGCCTTCTGGGAACCTATGGA
GAAAGGGAATCCAAGGAAGCAGCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCACCACATCA
CACTGCCACCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCCTATCCAC
CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCAGAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC
TGAGGGCCCCCTAGGGGCTTCTGTCTGCCCCAGGCTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT
CAGGGCTGCCCTTCACTGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT
GGGGTTCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG
TTGCATACATGCCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG
GATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

FIGURE 58

FIGURE 59

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGV DVRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMI EEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKV FVQTPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGT VNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP
```

TOH20T 1802T00T

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAGTCCA
GCCCCCTCTTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGA
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCGGTTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGACCAGGCTCTTGTGTCTCA
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGCTGGTGCTCATGGCACTTCCTCCTTG
CTCCACCCCTGGCAGCAGGAAGGGCTTTCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCAGACTCTGTC
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

104201-130400

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYGSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLIVIGDLLFSALWTFWLVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

FOH201-130-1001

FIGURE 62

[illegible]

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152

><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRLKGPDLHLASSCLWHLQGPDLML
KLRLEWTLAECRDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLTSTPYFSPSYSPQTHCSWHLTPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDGRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAACHCFQEDSMASVTL
WTVFLGKVVQNSRWPGEVSFKVSRLLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

[illegible]

FIGURE 65

[illegible]

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGT
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FOOTNOTES

FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCCTCCCCCGC
 TTCCCTGTTCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
 CGGCAAAGTTTGGCCCGAAGAGGAAGTGGTCTCAAACCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCG
 CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
 AGAAGAGTGCGGCGGCGGACGGAGAAAACAACCTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG
 CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
 CACCAGGGAGCCTGGGCGCCCGGGCTCCGCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG
 GCACCTCTGGACAGCCAGGATGCTGTGGCCACCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
 ACCGGATTATTTTCCAAATCATGCTGTGTAGGACCCCCAGCAGTGTCTTTAGAAGTGAGGGCACCTTACAGA
 GGCCCTGGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG
 TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCTACGCTCCCCTCTCCAGCCAC
 TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACTTACAGCTATG
 CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTCCTACAGCAAGATTGGCTGATGTGCCTGCAGGAAG
 AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT
 CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCTCCCTGCAATGCAATG
 TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCCACCCCAAGT
 CCTGCCATTGGCTGTGAGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG
 GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCAGTACTGCGTAGTCTCACCACCTTCA
 GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTACCACACAGTTGCTTGGAGCA
 ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCCTGTGGCTTAGGCT
 CTGGCCTGGGAGCTGGCGAAGGCTTAGGTGAGCGCTGTACAGTGAGGCAAGCGCTGTGACGGCTCATGGGACT
 GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGTGGCACCT
 CTGGTGCCACAGCCTGTACCTGCCTGTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA
 GACGCTGTCCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCCTGTATGAGACGTGGGTGTGCG
 ATGGGCAGCCAGACTGTGCGGACGGCAGTGTGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCATTACAG
 CTGAGTCATTGGCAGCCTAGTGTGCGGCTGTCTCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
 TTCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC
 CTTCTACGGGAGCTCATTGCCAGGGTGCATCCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATA
 ACTCAGTGTGGGCAACCTGCTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
 CCCGCCGTGCTCAGCGGGGCGCTTGATGCGACGCTGGTACGCGCTCTCCGCCGTGGGGCTTGCTCCCTCGAA
 CCAACACCCCGGCTCGGGCTCTGAGGCCAGATCCCAGGTACACCTTCTGCTGCTCCCCTTGAGGCCCTAGATG
 GTGGCACAGGTCCAGCCCGTGGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCACTGCCCATCA
 AGGCTCCCCTCCCCTCTGCTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
 TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCGCCTGTTGCCAGCCTGGGGCCCC
 CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCCGGCCCTGGAAGATGAGGACGATGTGCTACTGG
 TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
 CTCTACTGAGGCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACTTTTAGAGGTGGGTGAGCCTCCCCTCC
 ACCACTTCCCTTCCCTGTCCCTGGATTTTCAAGGACTTGGTGGGCTCCCGTTGACCCCTATGTAGCTGCTATAAAGT
 TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCCACTCCCT
 TCACCACCACTGCTCCCCACGCCACCACTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
 GGTCTGGACACTCCATCCTTGCCAAACCTTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA
 CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTGGCCATCCCAATCCCTCCTACAGGGCCTGG
 CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
 GGAATCATACTCTC

FIGURE 67

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCGDVDACGDGSDEAGCSSDPFPGLTPRP
VPSLPCNVTLEDIFYGVFSSPGYTHLASVSH PQSCHWLLD PHDGRR LAVRFTALDLGF GDAVH
VYDGP GPP ESS RLL RSL THF SNG KAV TVET LSG QAVV SYHT VAW SNG RGF NATY HV RG YCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPCADGSDEWDCS
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFP TENPN DNSVLGNLRSLLQILRQDMTPGGGPGARRRQGR LMRRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRL LPSLGPPGPTRSPPGPHTAV
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACCTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAAAGAAGTTTTGTAATTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

FOOTNOTES

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFVTVILFFILL
YVLRLDRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

100470044004

FIGURE 71

FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTIONTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTACATTACG
CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGCATTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCGTGACCCTGAGGTCGTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 72

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESNF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLR
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIIVLLLLPFRCL
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FOOTNOTES

FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGGAGCCGGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGCTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGAAGTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACCTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCTGAAGGCATGTGCCCTTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCCACTGTGCGGGACGTCTTGACTTCAAACGCCTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCACC
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTTGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCTGGGGAGGATGCTGAACCCGATGAAGACCCCACTGCTGAGGACTC
AGAGGCCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGCTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCGGGGCGG
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 74

FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAIVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNA
ISSCGRTREAFNLLLRVNHIGPFLTHLLLPCLKACAPSRVVVVASAAHCRGRDLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFLRHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAHRLWEASKRL
AGLGPGEAEPEDEDPQSEDSEAPSSLSTPHPEEPTVSQPYSPQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG
GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC
CAAGCCTCAGGCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCTGAGCATGGTGGCCCCAGAC
CCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGTGTACAGCCCCCTGCCCGGGACATGCCACGATGGCCAG
GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT
CGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG
TTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG
GCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG
ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCC
CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGAAAATGTGACACTGCTGAACCCGGAT
CCTGCAGAGGGCCCCAAGCCTAGACCGGGCGGTGTGGCTCAGCTGGAAGGTGAGTGGCCCTGTGCGCCTGCCCAA
TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC
GGCTGGCAGAGCGCAGAGCTTGGAGGCCTCCACTGGGGCCAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC
CGGGCTCGAGGCCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGAAAAAGTGCCAGTGCCCCACCTCAGGAA
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAATGGCATC
ATCCGTGGCTACAGGTCTGGAGCCTGGGCAACACATCACTGCCACAGCCAACTGACTGTAGTTGGTGAGCAG
ACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGTGGAGCT
GGGGAGCCAGTAGACCTGTCTGCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAGAACCCAGTGAGCAT
GGTCCCTGACCCCTGGAGCAGCTGAGGGCTACCTTGAAGCGCCCTGAGGTCAATTGCCACCTCGGGTGTGCACTC
TGGCTGTGCTTCTGGGCACCGCCGTGTGTATCCACCGCCGGCGCCGAGCTAGGGTGCACCTGGGGCCAGGTCTG
TACAGATATACCACTGAGGATGCCATCCTAAAACACAGGATGGATCACAGTGACTCCAGTGGTTGGCAGACACT
TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCCTCAGCAGTGGGCTGGGGGGGATGCCCGG
GACCCACTAGACTGTCTGCTGCTCCTTGTCTCCTGGGACTCCCGAAGCCCCGGCGTGGCCCTGCTTCCAGACACC
AGCACTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCAGGTCCCAGCT
GTCAGGCGCCTCCCACCCAGCTGGCCAGCTCTCCAGCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGCAGG
GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCTGCAGAGGCTTGAAGGCCAAAAAGAAGCAGGAGCTGCAGCAT
GCCAACAGTTCCCCACTGTCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCCCTGTGAGTTAGGAAATAGAGGTTCC
AAGAACCCTTCCCAAAGCCAGGAGCTGTGCCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCCTC
AGCTCCTCAAATGAGCTGGTTACTCGTCATCTCCCTCCAGCACCCTCTTTCTCATGAAACTCCCCAACTCAG
AGTCAACAGACCCAGCCTCCGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC
CTTAGCCCTGCAGTCCCCCTAGCCCCCAGGCTCTTCCCTCTCTGGCCCCCAGCCAGCTTCCAGTGCCTGTCC
AGTCCCTCACTGTCTATCCCTGGGGGAGGATCAAGACAGCTGCTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA
CTCAGTGAGGGTGAGGAGACTCCCAGGAACAGCGTCTCTCCATGCCAAGGGCTCCTTACCCCCCACCACCTAT
GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG
GGAGTCTTGCTGTGCCACCTCGGGCCCTGCCCTACCCCCACCCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC
TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGTCTCTCCGATGGCTCCTTCTCGCTGAT
GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCCGGTCTAGAGCCCAGGGAGGCAGACTGC
GTCTTCATAGATGCTCATCACCTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCCCTG
TGGGAGTGAGGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCCAGCGGCTGGGAAGGGGGATGCCTCCC
TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCACTCCACTGTCTGATGCCAAGGCTGGTGTCTCTCCT
GTAGATTACTCTGTAACCGTGTCCCTGAGACTTCCAGACGGGAATCAGAACCACTTCTCCTGTCCACCCACAAG
ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG
TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA
ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCACACCAGGTTGTTTTGGC
CTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCCACCATTGATCACAGGAAGTGGAGGAGCCAGAGGTGCCCTT
GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGAGCCCCCTCTCAGCCTTACCT
GGGCCCCCTCTTAGAGAAGAGCTCAACTCTCTCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTG
AGGCACTGAGGCCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG
TATGAGACCGTAGGTCAAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT
GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 76

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQGRHTVSGGSLLMARAEKSDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNLTLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSTPARPSPQVPAVRRLLPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANSPLLRRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
CCCTGCAGTGACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCTGTGGA
ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
TCTTTACTGATCTCTCTGTTTCGTCTTTCCAGGACCCTGCTGTCTCTCCCTCCCCTTCTCCAC
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCCAAGGCAAAGCTCAGCAAACCCAGCCCC
CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCCCCCCCATGCAGC
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTGCTGAGCCTTCTGTGAGC
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAAGGAAGCC
CCTTCCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
TCCAGCTGCCCCGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCA
GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTGAGGC
CTCATGCCCAGTGTGCGACCCCTGCCTTCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
GTGAAAAACGTGATTCTTGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
GACTCTGAATTCTAACAATGCCAGTGAAGTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTG
ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG
TCCAGGCCTTGGTCAGGTGAGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCCTTTGGAAAAAATGATGAAGA
AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
GCACAACTACTATTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT
GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG
TCTGGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTGTTTCAAGTATGCAAACTTGGAAG
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
TATTTCTGTTTGTGTTGTTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT
TTTACAGAGCAATTATCTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
ATCACTTTATCCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAAATGTTTCATCA
GCTGCATAAAAAAAAAAAAAA

FIGURE 78

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAE EEGQETMKGRVSIRD SRQELSLIVTLWNLTLQDAGEYWCGVEKRGPD ELLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

FOOTNOTES: 430200F

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGA CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCCCTGACCTAGGCTTGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

FIGURE 80

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD

YEADGSTNNGIFQINSRRWCNLTNPVNPVCRMVCSDLLNPNLKDTVICAMKITQEPQGLGY

WEAWRHHCQGKDLTEWVDGCDF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FOOT-180-FOOT

FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCTGCGTTC
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTCTGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTGTCTCCACAC
TCGACTCCTTGCCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACGAGTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG
GAAGGCCATCCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGTGCTTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA
GATACTGGTTGTATTTTTTGTCTGTTTTGGTTTTTGGGTCCTCATGTTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTGATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCAATTCAGCCCTTACATGGACAGCTAGA
GGTTTCGATATCTGTGGGTCCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCTGGAAGAGGAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCCCGAGTCACCTTTCACAGCGCTGTTCTCCATGAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCCGAGTCACCTTTCACAGCACTGTTCTC

Top201-1301-1001

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FOOTNOTES: 4802100F

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG
GTGCCCTGAAGGAGGAGGTCCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAAGTGCCTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTCAAGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAAGTGCTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAAGTGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

1304001

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGSSEEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVDCHSCSGTQAQLQTTRAEELGEAQAKLMEQESALR
ELRERVTOGLAEAGRGREDVRTELFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 85

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAAGTGGAGCCTCATTGGCCGGCCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCAGCCCGGCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCCAAGCAGTACCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTTCGGCGCCCCCGCTCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCTCTCCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTCTGCTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCCAGCCCGCCAAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCCGCAGCCCCCTGGGGCCCCCG
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGTGCTCCAGGAGATTGTCTTTCATCG
TCCAGGGGCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAA

FOOTNOTES

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFEAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFGVDSLDCGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA
NNGSPCPELEEEAECVPDNCV

Important features:

Signal peptide:

amino acids 1-26

FIGURE 87

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA
TATTGACAAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTAAGTCTAGGCGGA
CAGCTTTAGTGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTATTGAAAATA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT
ATCCAACCTTTGTTTGGGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCAATCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTGAGCAGATGAAT
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTGAAAAGAACCTGATGAGAGAAAGAAATTGCCAAAAA
TTAAAAAAGGACACAAGTGCGAATGT'FAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGAGTGAAGAGCTCAGAAAAGCAAGACAATTAAAACGGGAACCTTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAGCAGAAAAAAGAAAGTGAAGAGGAAGAA
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGAAGATCAGACCCTTGCACTGCTGAACCAGT
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATATAAAT
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAA

FIGURE 88

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAESEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKS
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK
QOSKKGTSREDOTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQSDTFEIIYDPRNPVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FOH20T 4304T00T

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCCG
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTTCGCTTGCTGACGGCGTCC
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTCCTTCCTTCGGAACGGGAACGTCTAGCAA
CCCTTCTGTGGGGCTCAATTTTGGAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
CTCCTTCAAGTGGTTTTTGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
GGAGGAACAAATACAGGTGCCCTTGACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCT
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAA
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCCAGGCTGGAG
TGCAGTGGCAGATCTCGGCTCACTGCAACCTCCGCCTCCCGGTTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG
ATGTACGTACGACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC
CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC
GAGAAAGTGGTGCTGGTGTTCCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTTCGGCCAGTCCGCG
GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGTCTCTTCCATCGGGC
CATTTCCAGAGTGGCACCGCGTTATTTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCA
GAACCTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAACCTGGAATTCATTGGCTCTTGCCCTTATAATATACCAAGGAGCAGGT
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGTGGC
TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC
TGACATCCCATGATGCCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTCCCTTCTTCAAATCCT
CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC
CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGCTCAACCTTGTTCCTGTCTGT
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTGGGA
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG
TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

1004254-1502400

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVFSPSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLVNYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLGCNHNSTQILVNCLRALSGTKVMRVS NKMRFLQLNFORDPEEI IWSMSPVVDGVVIPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
AGTCAGTGATGGTGCCGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCTACCCCCGA
CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
CAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC
GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAGTCTCCTTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTCACAGTACTTCTTTCTGGGTGGAGAGAGGAAGCTATGTGACATATAATTT
CATGAACGATGGGTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTTACGTGACAACAC
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGT
TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCGAG
AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCCG
GGTGAAGGCTGGGGATTGAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA
GCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA
AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCCTCGGGTT
CAAGTGGAGCACGAAGGAGAGTTTACCTGCCACGCTCGGCACCCACTGGGCTCCAGCACGT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTTCTCCAACGGAG
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAC
GATCCTGGATTACATCAATGTGGTCCCAGCGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
AAGCCACACCAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAG
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCCAGAACCCAAATCATCCACTCAAGC
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA
GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC
CAATGAGGGGTCTCTTAGGCTTTAGGACTGGGACTTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTGAGACACAGCCTG
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG
CGCCTGTAATCCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
AGGTTGCAGTGAGCCAAGATCACACCATTTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA
TCTCAAAAAAAAATCCTCCAAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA
AGGTGGGTGGATTGCTTGAGCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC
ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCGG
TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA
ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTGCCTCACTGCTACACTCCT
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA
GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTGTCTATGGAGTAGCCATTCTTTTGTTCCTT
TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAA

104201-1502001

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAGNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSHWPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQSPDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNOQATPNSPRTPPPPGAPSPESKKNOKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPQVRPRPEARMPKGTOADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins
signature.**

amino acids 365-371

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGCTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTCAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAAGCTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTTCGCAAACATTTGACATTATTACTAATCATGAAACTCAAGAAGGAATAGTTATATTTAA
AAAGAAAGTGGATTTTGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCAATTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTTGCTATTCTCATTTCATTATGATCATA
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCTGA
GAAAAGTGAAGATTTCAAGAGAGAATATATTCATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTTTACCATCAAATTTTTTAAAAGTGCTAATGTGTATTGGAACCAATGGTAGTCTTAA
AGAGTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATAATG
TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCTTTAT
TTAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYVVFEEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHFHYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPD SAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGS LAGSLSSLES AVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 95

FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGATTAATTAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTGCGCAAACATTTGACATTATT

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTTCTCCGCGGGG
CCCAGCCACCTTCGGGAGTCCGGGTGCCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCATGGCCAACGCGGGGCTGCAGCTGTTGGGC
TTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG
GATTTACTCCTATGCCGCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGA
TGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCATGACCCTATGACCCCACT
CAATGCCAGGTACGAATTTGGTCAAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCCC
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGGAAAGACTACGTGTGACCACAGAGGCAAAAG
GAGAAAATCATGTTGAAACAAACCGAAAAATGGACATTGAGATACTATCATTAACATTAGGAC
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCCCTCA
ATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA
ATAGACAGTAAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAAATATCTCTAAAT
AGGTAAATGTATTTAATTCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC
TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTTA
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAAATCTTTCTGCATG
ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
AACACAACCTTTATTGATTGAATTTTTAAGCTACTTATTATAGTTTTATATCCCCCTAACT
ACCTTTTTGTTCCTTCCCTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTTA
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT
CACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC
CTTCATGTGGCTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCATTCTTTCAGCTGTGTCT
GACATGTTTGTGCTCTGTTCCATTTTAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAATTCCTGATCTTCCCACCTCACAGTGATG
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAGTGCTAT
ACTAAGGGAAAGAATTGAGGAATTAAGTGCATACGTTTTGGTGTGCTTTTCAAATGTTTGA
AAATAAAAAAATGTTAAG

1041207-1302E007

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI~~L~~AWIGAI~~V~~STALPQWRI~~S~~YAGDNIVTAQAMYEG~~L~~WMSCV~~S~~QSTGQI
QCKVFDSL~~L~~NLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTPV~~N~~ARYEFGQALFTGWAAASLCLLGALLCCSC
PRKTT~~S~~YPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 98

FIGURE 99

[illegible]

FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGACGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

FOOT-480204

FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTCGCAGANCACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCCTGCGA

TOP SECRET 4804 FOOT

FIGURE 102

ATTCTCCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCTCTGTCCC

FIGURE 102

FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCAATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC
CCTACTTTGCTGTTTCCTGTCCCCGAA

FIGURE 103

FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA
ATTTTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTTCCTGCGAACC

FOOT-4802

FIGURE 105

TCATAGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTTGCTGTTCTG

TCATAGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA

FIGURE 106

TTCCTGGGATGGATCCGCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCCTATGACCCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

404207-1802400F

FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA
CTGCCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCCTGCGAA

FIGURE 107

FIGURE 108

TCGTTGGTGTAAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC
TCTTAAAATGACACCCCTTCCCTCGCCTGTTGGTGTGGCCCTTGGGGAGCTGGAGCCAGCAT
GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGGCCACTCCCGGCCAGGCTG
CTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTTCACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAATGTTATTTCAGAGATGTTTAAATGCATA
TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTACAAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA
GGAAGTGTTTTTCTGGGTCAGTAAATAACAATGTCTATAGGGAGGGAAATTCTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHCLKFRGPFTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQFDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRCVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMRTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 109

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAATTATAATAAAGCC
CCAAAATTAAGAATTCTTTTGTCATTTTGTACATTTGCTCTATGGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAATGAGC

FOOTNOTES

FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

FIGURE 111

FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

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FIGURE 113

GGTGGCCCATTCCTGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTCAANTTAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACG
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

TTTGTGAGAGT

FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTTCAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

FOOTNOTES

FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACCNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCAANTCCC
GGCCCAGGCTGCTTTCCGTGTCCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCAANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTTC
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

FOOTNOTES

FIGURE 117

CGGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCGCCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTTCACTGCCA
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTTACC
CCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCAGC
CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCACTATCTTGGACAAA
AGGTTCTTAACCAATTTCCCTTTTCAACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGTC
AGAGGATTGCCGAAGGGAGGCCTTCTTTTCACTGGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA
TGCCTGGTGGAAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGCACTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAGAATTGGAAGC
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTTCAAGAGGAC
TACAACGTTGCTGTTTCGCATCACTCCCTAAATACGCCCAGATTTGCCTCTGGATTACGG
GAACGATGCCAATTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT
GAACTCTGTCAATAGCATTTCAACATTTTCAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
CATGGTGTGAGTTTTCATTTGTAGAAAAATTTTGTGTCCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
GGGACATTTAGTTTGTGTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA
CAAACTAATAACTGTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTTTAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTTCTGATTAG
TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRFLTNPFFSTAVKLSTGCSGILISPQHVLTAHCVHDGKDYVKGSKKLRV
GLLKMRNKS GGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDENDDLQYCYDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNAVVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCAACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGGTTGCACCTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCTTGATCACTT
ATATCTGGAAACCAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTGTAACCTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCCAAAACAAAGCCCCACATAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGTCAGAGGAGCCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPCSLKCQ
AKGTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSLSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQAELEEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCCGGTTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGTGCCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGACTCCTCAAAAGTTCAGCTCCCAGCA
GGATTGTGGTAGTTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGGAGCAAAGTGGCTAACATTCTTTT
TACCAGGGAAGTAGCCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC
AATTTGGTGTCATGGGCTTTTTTCAAACTCCAGTAGAAGGTGCCCAGACTTCCATTTATTT
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAAGTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAAAGTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGAGTTACTGAAAATTATTTT
TGGGATAAGAGAATTTTCAAGCAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATA
GTACAATGAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTCAGAATTAAGTGAAGTCAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

Top201-180CT001

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRRELRLQAEECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANILFTRELARRLEGTVNVTNVLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAAATTATCTGCCTGGCTT

FOOTNOTES

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGAGCCCAGCC
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC
CCCAGCGTTACCAATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCATTAAGGAAGAATT
TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTTCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTT
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCTTGGAAGCAATTCG
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCAGTGAAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAACTTG
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAIEITTLDRSKRNIIGYFEQKSDSNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEEELTEEGLPFLILFHKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPRESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

104207-480400F

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCCGCCGCGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCCCTTTCCTAACCC
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGCTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

FOOTNOTES

FIGURE 128

CCCCACGCGTCCGATGGCGTTCACGTTTCGCGGCCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCCTGAATCCCCCTGTACTCCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA
CTCTATGACCCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG
TTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAACCTGCACCTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACCTTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGT
GCAATACAATAAACTCTGAAATTAAGACTC

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG
AATCCCCTTGTA CTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
T TACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

FIGURE 130 FOOT

FIGURE 131

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC
CTACCCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGTTGCCAGAATCAGCTGCC
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAACCTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATTCCTCCTCATAGAGCTTTTAAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

101201-130200F

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLT MALAGGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYP
KEEELYACQQRGCR LFSICQFVDDGIDLNRTKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHL LFP LTLVRSFWSDMMDSAQSFITSSWTFY LQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

FOOTNOTES

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC
TGAAGTGAAGACAAGACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

[illegible]

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGCGCGGAGGTTGCGGGACCG
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

total = 1302

FIGURE 135

CGGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCCGACGGGCTTCATCTGAGGGCGCACGGCCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCGCGGCTG
GGGATTCTTGTGTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAAGTGTTTTAAGCCAC
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAATAAGGGCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG
CATTTTGATGAGAATTCATTTTTTGCTGGGGATAAAAAAGAAGCACACAACTAAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGACCTAGTTATGAATTCCATCTAACCAGACAAGA
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAT
TCAGGAACCTTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCGTGTTTCTGGAC
AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAGGAGAATTATATTGTTTTAAGTAAACACATTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAARCFQCQVSGYLDDCTCDVETIDRFNNYRLF
PRLQKLLESDFRYYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVDPDGIKSASYKYSEEA
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALSKVLPFFERPDLFQFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTOGLGTALKILFSEKLIANMPESGPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAA
TGTTACTTTTGGAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

FOOT-4804T0120

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACCTCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCTATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCAAGCCTGGGAGTAACTATTTCCCCCATCCCAGGCCTGTGCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPLRFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW

DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

protein database

FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCCTTCCAACTTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAAGTGGGAAATTCATCTCATCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGTGG

FIGURE 140

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTTCGTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
TGGTCCCTCCCAGACACCTTGAAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAAG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
CTCATAGGTTTTCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGAAGTGGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTCAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCCTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTCACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTACAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAA

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLEFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLIMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDDITATVPYNLRVRATLGSQTS
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPVLALFAFVGFMILV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCTAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT

FIGURE 144

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGACAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGC GGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG
AGGTGCAGCTCATTCACTTCAACCAGGAACCTACGGGAATTTAGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCT
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGC
AACAGGGACCCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA
TGGTGTCCCCCATGGTCGCTGAGACTCCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAACAAAGCTATTAAAGGGACAGAATACTTA

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLNRTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE
TVTWILIDRALNITSLOMHSRLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

FIGURE 146

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCCGCCAGCCTCCGCCGCCGAGCCTC
GTTTCGTGTCCCGCCCCCTCGCTCCTGCAGTACTGCTCAGAAACGCTGGGGCGCCCCACCCTGGCAGACTAACGAA
GCAGCTCCCTTTCCCAACCCCACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCAGGTTGAGGGAGC
CGCAGAGGGCGGAGGCTCGCGTATTCTGTCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCT
CACCTCTCCCAGGAACTTCACTGAGAGCCAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
ATCCTGAGGTCAATCATTATGAAGTGTACCGCGCGGAGTGGCTCAGAGTAACCACAGTGTGTTTATGGCTAGA
GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
TTGGGAGCACACTGGGGAAGATATAGGCCCCGACGTTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTT
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTGAGGTGTTCTGGCCCTGTATGTACACATTATACA
CAGGTGCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTACATAACATGAACATCTGGGGGCAG
ATATGGCCCCAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAGGGAACTGGTGGGGCCATGCCCTTACAAA
CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTGGAGGGGGCTGTAGAGAAAATCTGTCTACAAAGAGGG
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCCACAGCAAAATGTCCCAAATTGTTTCT
TGTGAAGTAAGATTAAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGAT
AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCAATTATGGT
ATAATAGACAAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA
AATGGTATTCAACAATGGCAAATATCAGTCTGCTAATTTCTTCACAGTCTCTAAAGTAACAGTTTCAGGCTGTG
ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCCAAGAGTATACTGTCT
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATGGAACTCGAGTTTATTCTGATCTGTCCAGTATC
TGCAGAGCAGCAGTACATGCTGGAGTGGTTGCAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
AAGACCTACATTGCTTCTTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATTC
AGAGTGTGTTGCTGTTGTGTAAGTGAATACTTGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
ATTTTGTATAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTCAGCCCCAAAAGGTGCCAAATGCATA
TAAATCTTGATAAACAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
GTTCTACGTTTCATATATTATATGGTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACCTGAAAGAAACCTTATCACATTTTCCCC
AGTTCAATGCTATGCCATTACCACTCCAAATAATCTCAAATAATTTTCCACTTAATACTGTAAAGTTTTTTTC
TGTAAATTTAGGCATATAGAATATTAAATCTGATATTGCACCTCTTATTTTATATAAAATAATCCTTTAATATC
CAAATGAATCTGTAAAATGTTTGATTCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
ATGAAAACATTCCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
AAATTGAGGTCACATATTTTCTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
GAACAAAGATGAACTAATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTGTATATAA
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA
AATCTGTAAAATGTTAGTTTTGGTAAATTTTTTTCTGCTGGTGGATTTACATATTAAATTTTTTCTGCTGGTGG
TAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAA

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEK LLEKYMDEEDGEW WIAKQRGKRAITDNDM
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLC
HNMNIWGQIWP KAVYLV CNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRY
YPPREEETNEIERQQSQVHDTHVRTRSDSSRNEVISAQQMSQIVSCEVRLRDQCKGTT CNR
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGI
QTIGKYQSANSFTVSKVTVOAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCCGCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCTGCTCCCACGCCC
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA
CTTTGCAGATTAAAGCCTTTC
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAA
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTTGCTCCATTCCCTAGCTTGGGAAGC
TTCCGCTTAGAGGTCTGGCGCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCATGTAATTCTTCAATGTAAACAGTGCACTCCTCTTTCGAAAGCTAAGAT
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAAA

FIGURE 149

MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE

Signal sequence:

amino acids 1-34

[illegible]

FIGURE 150

CCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCGGTCTGCGTCATGTTAAACTCCAATGTCCTCCTGTG
GTTAACTGCTCTTGCCATCAAGTTTACCCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG
CAAAATCCGGGGCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA
TGCCTACCCCCCACTGGAGAGAGGCGGTTTCAGCCCCAGAACCCCGTCCTCTGGACTGGCATCCGAAATAC
TACTCAGTTTGCTGCTGTGTGCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT
TACCGCCAATTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTTAAACATCTACGT
GCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA
TATTCATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA
CATGATTGACGGCAGCATTTTGGCAAGCTACGGAACGTCATCGTGATCACCATTAACTACCGTCTGGGAATACT
AGGGTTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG
GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC
CTGTGTCAAGCCTGTTGACCTGTCCCCTACTCAGAAGGTCTTTCCAGAAGGCCATCATTAGAGCGGCACCGC
CCTGTCCAGCTGGGCAGTGAATAACAGCCGGCCAAGTACACTCGGATATTGGCAGACAAGGTGGCTGCAACAT
GCTGGACACCAAGGATGGTAGAATGCCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC
GGCACCTTACCACATAGCCTTCGGGCCGGTGATCGACGGCGACGTATCCAGACGACACCCCGATCCTGATGGA
GCAAGGCGAGTTCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCTGAAGTTCTGTGGACGGCAT
CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCGGTGTCCAACCTTCTGGACAACCTTTACGG
CTACCCTGAAGGGAAAGACACTTTGCGGGGAGACTATCAAGTTTATGTACACAGACTGGGCCGATAAGGAAAACCC
GGAGACGCGCGGAAAAACCTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCGCGGTGGCCGCGGACCT
GCACGCGCAGTACGGCTCCCCACCTACTTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCAGCTG
GGCAGATTCCGGCCCATGGTGATGAGGTCCCTATGTCTTCGGCATCCCCATGATCGGTCCCACCGAGCTTTCAG
TTGTAACTTTTCGAAGAACGACGTATGCTCAGCGCGGTGGTCTGACCTACTGGACGAACCTTCGCCAAAACCTGG
TGATCCAATCAACAGTTTCTCAGGATACCAAGTTTCAATTCACACAAAACCAACCGCTTTGAAGAAGTGGCCTG
GTCCAAGTATAATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAACCCAGAGTGAGAGATCACTACCGGGC
AACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCTCATTGCAAACTTGAACGAGATATTCAGTATGTTTCAAC
AACCACAAAGGTTCTCCACCAGACATGACATCATTTCCCTATGGCACCCGCGGATCTCCCGCCAAGATATGGCC
AACCACCAAACGCCCAGCAATCACTCCTGCCAACAACTCCCAAACACTCTAAGGACCTCACAAAACAGGGCCTGA
GGACACAACCTGTCTCATTTGAACCAAACGAGATTATTCACCGAATTAAGTGTACCATTGCCGTGGGGCGTC
GCTCCTCTTCTCAACATCTTAGCTTTTGGCGCGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACTCACAG
GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCATATCCAGAACGAAGAGATCATGTCTCTGCAGAT
GAAGCAGCTGGAACACGATCACGAGTGTGAGTCTGTCAGGCACACGACACACTGAGGCTCACCTGCCCGCCAGA
CTACACCTCACGCTGCGCCGGTCGCCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA
CACACTGACGGGGATGCAGCCTTTGCACACTTTTAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
CGGACATTCCACCACTAGAGTATAGCTTTTGCCCTATTTCCCTTCTATCCCTCTGCCCTACCCGCTCAGCAACAT
AGAAGAGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAGAAAGTCTCCAGACCAGGAATGTTTTTGTCCCCT
GACTTAAGACAAAAATGCAAAAAGGCAGTATCCCATCCCGGCAGACCTTATCGTTGGTGTGTTTCCAGTATTAC
AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTTAAAATAACTGCTTTAAGATCTCTACCA
CTCCAATCAATGTTTAGTGTGATAGGACATCACATTTCAAGGCCCCGGGTGTTTTCAACGTCATGGAAGCAGCT
GACACTTCTGAAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGAAGTTTAAACATTTCTTTCTGTGC
CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGCCAGCACATGGAGCTGTAATCCAG
AGAGAAGGAAACGTAGAAATTTATTATTAAAAGAATGGACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAGAG
GTGTTTTGCCAGCCTGAACATATTTAAGAGACTTTGT

FIGURE 151

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN
EDCLYLNIIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTSLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMNL
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSWADSAHGDEVPYV
FGIPMIGPTLFCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPPDMTS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTEISVTI AVG
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

FIGURE 151

FIGURE 152

GGGAAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTGTTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCTGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG
GTGCCATGTTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCTGGTGATTCTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCCTTGAAGTTGTTTGAAGTGAAGTGGAGAGAACCCCAAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCCTGGCCCTCTTCCTCATCGTCTTTTTCTCCCTGGTGTCTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCACTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCATG
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCTATGGTTGTGCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAATCACAGAAC
AGAATTTCATAGCCCAGGCTGCCGTGTGTTTGAAGTCAAGAGGCCCTTCTACTTCAGTTTTG
AATCCACAAAGAATTAAAACTGGTAACACACAGGCTTTCTGACCATCCATTCTGTTGGGTT
TTGCATTTGACCCAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAACACAGGATGGAACT
TCTTCCCTGCCTTACCTTCCTTTCACTCCATTATTGTCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTGGGGCTGGGGCTGCAGAACACACCTGCGTTTCAC
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCTGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT
TACGATTTTGGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT
CACTGTCAATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCCTGGAAGTCTGAGTCTCCTATGAACCTCTGTAGCCTAAATGAAAT
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLGMNAMVMTQYIRLTPDMQSKQ GALWNRVPCFLRDWELQVHFKEHGQGKKV
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKL FELTVERTPEEEKLHRDVFLPSVDNMKLPMTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

FOH2DT-H30CT00T

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
 CTGATGGTGGGTGCTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCAATTCAAGAAT
 TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAATCTGTTTTCTAGAAGAGGTTAATTAATGCCCTGCAGTCT
 GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTTCCGCAACCGCTTCT
 TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT
 CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCTGTGACGGAGCCCCCTGTGA
 CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCC
 CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTCATTGCCACGGAGACAGGTACCCACTGTATGTCTATTCCCA
 AAACAAAGCGACCAAAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAATGGAAGCTTTCA
 TTAGTCACATGTCAAAAGGATCCGGAGCCTCTTTCGAAAGCCCTTGAACTCCTTGCTCTTTACCCAAATCACC
 CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTCAGAACGGTCAGCTGCTGAGGGATA
 TCTATCTAAAGAAACACAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA
 GCCGGACCCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGAAGTGAAGAAGATTATTTCA
 GGCACAGCCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACAGTATCTGGAAAAGGAGC
 AGCGTCGTGCTAGTCTCCTAGCTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG
 ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTGAGCT
 TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGAAGAAATGTACTTCGGGTATTCTCTCCTGGGTGCCACCCATCCTGAACCAACCATCG
 GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAGAGCTCTTGGCCCTCTACTCTGCTCATGATGTCACTCTGT
 CACCACTTCTCAGTGCTTTGGGCTTTTCAAGGCCAGGTTCCCAAGGTTTGACGCCAGGTTGATCTTTGAGCTTT
 GGCAAGACAGAGAAAAGCCAGTGAACATTCGGTCCGGATTCTTACAATGGCGTCGATGTACATTTCCACACT
 CTTTCTGCCAAGACCACCAAGCGTCTCTCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAA
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTACAGGGAAGGATTCTAAAAGG
 TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAGGTCCTTCTAGTTTTGTCTGTTAC
 TAAGGTTAGAAGATTATTGCTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGGTTGGGGTTGAACAGT
 AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT
 TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
 TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTAAATCTTAGACATT
 TTTACCTTGTCTTGTAAAGATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTTCTGTAAAGG
 GCCAGATTGTAAATATTTAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTATAACTACTCAACTCTGT
 TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA
 GATGGTGACCAGACTTGCCCTGGGCTGTAGTTTGTCTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC
 ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACCTCTGCTAGAAACA
 CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
 AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTAAAGTATGTTCTAAATATTTGT
 CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTGTATGCCATTTAGTATTTTATAGTTTATAGAAAATATT
 TTCTAAGACCAGTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
 GAGGCTAGAAGATGAATTCAGGCACCTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA
 ACTGGATTCAATTTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTCTGATTGATTTTTAAATGCGTTTTTGGGA
 AGAATTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTATATATTAGAAGCAATTATAATTACATCTG
 TGATTTCTGAACTAATGGTGCTAATTAGAGAAATGGAAGTGAAAGTGAGATTCTCTGTTGTCTATCGGCATTCC
 AACTTTTTCTCTTTGTTTTGTCCAGTGTGCTTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

FIGURE 154

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALAAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPSPAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLLLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMMLCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF
CQDHHKRSPKPMCPLNLVRFVKRDMFVALGGSGTNYDACHREGF

protein head

Signal sequence:

amino acids 1-18

[illegible][illegible]

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRY SFRYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTS LASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYSLVTDI VLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVS LVSVTAHDPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVA VDRDSGQNAWLSYRLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVVAVAAVSCVFLAFVILL LALRLRRWHKSRLQASGGGLTGAPASHFVGVD
GVQAFLQTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFFNC SVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLWEAEAGGSPEVGSLRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

CCAGGCTCTAGTGCAGGAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTGTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTT
ACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTTCACTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTACCCAGTCCCCGAGAGAATTTTCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT
CTGGTTC

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWWLTAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

FIGURE 160

GGCGCCGGTGACACGGGCGGGCTGAGCGCCTCTGCGGCCGGGCGCTGCGGCCCGGCCCGCGCGCCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCGGGCCCCGCGCCCCGCGCCCGCGCCAGGTGAGCGTCCGCCCGCCGCGAGGCCCGCCCCGGCCCCGCCCCGCCCCGCCCCGGCGGGGAACCGGGCGGATTCTCTCGCGCGTCAAACCACCTGATCCCATAAAACATTATCTCTCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCCGCCGCCCTCGCCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGCGGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCGGGGCGGGCCGTAGCGGCGGGCGCCTGGA

TGCGGACCCGGCCGCGGGGAGACGGGCGCCCCGCCCCGAAACGACTTTTCAGTCCCCGACGCGCCCCGCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGAGCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTGCTGCCAGCCAGCGCATCTTCTGACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC

CGTGCTGCGCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATCGGCTGCCTTCACTGGCCTGGCCCTCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCTGECACATTCCACGGECTGGGCCGCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACACCTCTTCTGACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTTCCGTGACCTTGGCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCACTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCCACTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCCGTGACCTCAAACGCCTAGCTGCCAATACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACCGATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCCGGTGACAGCCCCGCGGGCAACGGCTCTGGCCACGGCACATCAATGACTACCCCTTTGGGACTCTGCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCGAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCTTGGGCCCTGCTGA

CCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCCACGCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAGGCCAGGTCCTCTCCTGATGGACGCTGCGGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGGTTTCGGCGCAGCGTTTGTTCCAGAACGCGCCTCCACCCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA

AAAA

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHG NRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLHTLHLDRCLQELGPG LFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP
LRALQYLRLNDNPWVCD CRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

[illegible]

GGAGATCCACGCGGGAGCTTGGATGTCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCAAGCCTCAGATACTGGGGACTTTAC
AGTCCACAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTCTCTTTCTCTTTGGGCTTATCTCTGGCG
GGCGCGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTAGGGTTG
TTTCCAGAGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAACAAATATTGAGAACTA
TATAATCAGCCCAACTCCTATTTTTCGGGTCTCACC CGCAAACGAGTGATGGCAGGAAAT
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
AGGACAGTCCGGTAGGCTTCTGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
AACGGAGAGATTTCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT
CAATCCCTTGACAGGAGAAATGAACATAAAAAACAACCTCGATTCGAAAACTTCAGTCTT
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTCTGGAAATGCACCGTTCTGATT
CAAGTGATAGATGTGAACGACCATGCCCGAGAAGTTACCATGTCTGCATTTACCAGCCCAAT
ACCTGAGAACCGCGCTGAAACTGTGGTTGCACTTTTCAGTGTTCAGATCTTGATTAGGAG
AAAATGGGAAAATTAGTTGCTCCATTGAGGAGGATCTACCCTTCTCCTGAAATCCGCGGAA
AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGGAGAAAGCAGAGCGGAATACAACAT
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTACCCAAACCTCTACACCCTGTTTCGTC
CGCGAGAACAACAGCCCCGCCCTGCACATCCGCAAGCTCAGCGCTACAGACAGAGACTCAGG
CACCAACGCCCAGGTACCTACTCGCTGCTGCCGCCCCAGGACCCGCACTGCCCTCACAT
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCTCTGGACTACGAG
GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG
CGAGGCGCTGGTGC GCGTGGTGGTGCTGGACGCCAACGACAACCTGCCCTTTCGTGCTGTACC
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTAC
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTTCGTACCA
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGCTGGTCAAGGAC
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGAGCGGCTTCTC
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGACCCAGGCCAGGCCGACTTGCTCACCG
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTTGGTGCCCGA
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCAGAGCTACC
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTTCTGAAGCCGATT
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA
TAACCTTTGGGTTCAATATTCAGTGACCATAGTTGACTTTTTACATTCCATAGGTATTTTATTT
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT
TTACTCTTGATTTTTTCTCATGTTCTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
CCTGGTTCTT

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTPCVLRQVLLESPPFEFFQAEQV
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVTGNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAEVMTSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPMLITQ
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFLGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAO
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

FOOTNOTES

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

Figure 1 consists of 12 histograms, labeled (a) through (l), arranged vertically. Each histogram shows the frequency of a specific number of contacts (x-axis, 0 to 10) for a given distribution. The y-axis for all plots is 'Frequency' ranging from 0 to 10. The distributions are as follows:

- (a) Uniform distribution: All contact numbers from 0 to 10 have a frequency of 1.
- (b) Distribution peaked at 1: Frequencies are 1 for 0, 10 for 1, 1 for 2, and 0 for 3-10.
- (c) Distribution peaked at 2: Frequencies are 1 for 0, 1 for 1, 10 for 2, 1 for 3, and 0 for 4-10.
- (d) Distribution peaked at 3: Frequencies are 1 for 0, 1 for 1, 1 for 2, 10 for 3, 1 for 4, and 0 for 5-10.
- (e) Distribution peaked at 4: Frequencies are 1 for 0, 1 for 1, 1 for 2, 1 for 3, 10 for 4, 1 for 5, and 0 for 6-10.
- (f) Distribution peaked at 5: Frequencies are 1 for 0, 1 for 1, 1 for 2, 1 for 3, 1 for 4, 10 for 5, 1 for 6, and 0 for 7-10.
- (g) Distribution peaked at 6: Frequencies are 1 for 0, 1 for 1, 1 for 2, 1 for 3, 1 for 4, 1 for 5, 10 for 6, 1 for 7, and 0 for 8-10.
- (h) Distribution peaked at 7: Frequencies are 1 for 0, 1 for 1, 1 for 2, 1 for 3, 1 for 4, 1 for 5, 1 for 6, 10 for 7, 1 for 8, and 0 for 9-10.
- (i) Distribution peaked at 8: Frequencies are 1 for 0, 1 for 1, 1 for 2, 1 for 3, 1 for 4, 1 for 5, 1 for 6, 1 for 7, 10 for 8, 1 for 9, and 0 for 10.
- (j) Distribution peaked at 9: Frequencies are 1 for 0, 1 for 1, 1 for 2, 1 for 3, 1 for 4, 1 for 5, 1 for 6, 1 for 7, 1 for 8, 10 for 9, and 0 for 10.
- (k) Distribution peaked at 10: Frequencies are 1 for 0, 1 for 1, 1 for 2, 1 for 3, 1 for 4, 1 for 5, 1 for 6, 1 for 7, 1 for 8, 1 for 9, and 10 for 10.
- (l) Very narrow distribution: Frequency is 0 for 0-4, 10 for 5, and 0 for 6-10.

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC
 GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT
 GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG
 AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
 GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
 AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
 TGATTCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
 GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
 AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
 CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
 GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT
 TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT
 GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
 CACTTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
 TGTTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
 GAACACTGGAAACACTGAAAATCTTCATTTTAAATCAGACAGGTATAGAAGCCAAGAAGAAT
 GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA
 CTGGTTGCTTGTATTTTCTTATTCTTTTAAATTAGTTTATTATGTATGCTACCATTGAA
 CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
 GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
 CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA
 CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
 AAAAAATATTCAATAG

FIGURE 165

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333
><subunit 1 of 1, 360 aa, 1 stop
><MW: 39885, pI: 4.79, NX(S/T): 7
MVPAAGRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMAFNHTDRTLETLETKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLSLFFLISFIMYATIRTESIRWLPQGQEHVE
```

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

Protein = 1202 TOOT

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGGGGCTCTTCCTC
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGACAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCTGGCCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGACGTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCCGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTTACCTAAAGGAAAAGCCACCCGAATCTTGTAGAAATATTCAAACATAATA
AAATCATGAATATTTTAA

FOHET-480ZT001

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGLLLLLFLASHCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDLDETIQPCHS LCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSE RDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGGELVITSVKRWQKGQREFKRISRSIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

FIGURE 167

FIGURE 168

[illegible]

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPVLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQIQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAEGILIMLMTALTVRSEPSLSTCQQGEDPLDWTVSLLL MAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

protein=1602700

FIGURE 170

GTCCACATCCTGCTCAACTTGGGTGAGTCCCTCTTAGACACGACTCTTGTCATCATTTGCTGAAGTGGAACCAAC
TAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCGCGGCAGCTCTGGGGG
AAGGAGACCGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAATCTTAGTGGTT
TCTGAATCTAGCCCACTTGGCGGTAAAGCATGATGCAACTTCTGCACTTCTGCTGGGCTTTTGGGGCCAGGTGC
CTACTTATTTCTTTTAGGGGATGTGAGGAGTGACCACTCTCACGGTGAAATACCAAGTGTGAGGGAAGTGGC
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCGGGAGGAGAGCGGAGGCAAGCTTGGGGCCGCCCTT
CCAGGTGTGTCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTCTTGATGTGCTTGCCAAGGGGATTT
GGCTCTGATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACAGGCCAGGTTTCCCAAAGGCGAGCAGG
GCTGGAATCTCTGAGAGCGCTCTCTGCGAACCCGATCCCTCTGGACAGAGCTCTTGACCCAGACACAGGCC
TAACACCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCTTGGATGTCTGTTGGGCGCTGATGAGAC
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCAATTTTTGATCTGGTGTAACTGC
CTATGCAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGCTTTGGACTCCAATGACAATAG
CCCTCGCTTGTGATGAGATTCAAGTCTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT
GACCGCCACAGACCTTCCAAGGCCCAATGGGGAGGTGGATTTCTCTCAGTAAGCACATGCTCCAGAGGT
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTGCACCTCTAGACTGAAAAAGAACCC
TGCTTACGAGGTGGATGTTGAGGCAAGGGACCTGGGTCCCAATCCTATCCAGGCCATTGCAAAGTTCTCATCAA
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTACATGGGCTCCAGCCATCACTGGTGTGAGAAGC
TCTTCCCAAGGACAGTTTATTTGCTCTTGTGATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG
CTGGCTGAGCCAAGAGTCTGGGCACTTCAGGCTGAAAGAACTAATGGCAACACATAGTTGTCTAACCAATGC
CACACTGGACAGAGAGCAGTGGCCCAAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCAGCCCTTATC
AGCCAAGAAAACAGCTCAGCATTAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGA
AGTCTCCACGCGGGAACAACTTACCCTCTCTTACCTCAATACCATCAAGGCTCATGATGCAGACTTGGGCAT
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCAAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
GGTCACTGCTCAGAGTCACTGAATATGAAGAGTGGCCGGCTTTGAGTTCCAGGTGATGCGACAGGACAGCGG
GCAACCCATGCTTGCATCTCAGTGTCTCTGTGTGGGTGAGCTCTTGGATGCCAATGATAATGCCAGGAGGTGGT
CCAGCCTGTGCTCAGCGATGGAAGGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGC
CATCGAGACTCCCAATGGCTTGGGCCCAGCGGCCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCCTCTACAGCATCCGCAATGG
AAATGAAGCCCACCTCTTCACTCTCAACCTCTATACGGGCGAGCTGTTGCTCAATGTCAACATGCCAGCAGCT
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT
GAGGGTCATGTTTGTACCAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT
GCTGACGGTGATCTGCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCTGGCTTTGTTTATGTCCATCTGCCG
GACAGAAAAGAGGACAAACAGGGCCTACAATGTCTGGGAGGCGCCAGTCCACTACCCGACAGCCCCAAGAGGCC
CCAGAAACACATTCAGAGGCAGACATCCACTCTGCTGTGCTCAGGGGTGAGGAGGTGAGCCTTTGTGAAGT
CGGGCAGTCCCAAGAGATGTGGACAAGGAGCGATGATGGAAGCAGGCTGGGACCCCTGCTGTCAGGCCCTCT
CCACCTCACCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGT
GCTGCAAGACACGCTCAACCTCCTTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGAGAACCTGAACCTTCC
CGAGCCCCAGCCTGCCACAGGCAGCCAGTTCAGGCCCTCTGAAGGTTGACAGGCAGCCCCAAGGAGGCTGGC
TGGAGACAGGGCAGTGAGGAAGCCCCACAGAGCCACCAAGCTCTCTGCAACCTTGAGACGGCAGGCAGCATCT
CAATGGCAAAGTGTCCCCGTGAGAAAGATCAGGGCCCCGTGAGATCCTGCGAGCCTGGTCCGGCTGTCTGTGGC
TGCTTTCGCCGAGCGGAACCCGTGGAGGAGCTCACTGTGGATTCTCTCCTGTTTACGAAATCTCCAGCTGTCT
GTCTTGTGTCATCAGGGCCAAATCCAGCCCAAACCAACCACCGAGGAAATAAGTACTTGGCCAAGCCAGGAGG
CAGCAGGAGTGCAATCCAGACACAGATGGCCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCACTGCTAGAAGAAAGAGCTCAAGTCTGCTGGACCC
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCCCTGACCCGCGCTGATGGCGAGACTCTTTTGGCCCTCAC
CACCACCTACCGTGACAATGTGATCTCCCGGATGTGTCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG
CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCGCTGGAGGCGGCTCCGAGGCGCTGCGGCGGCTCTCGGT
CTGCGGGAGGACCTTCAGTTTAGACTTGGCCACAGTCAGCCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG
AAAGACGGGGACTGAGGCAAGAGCAGGACAGGCAGCAGCAGCAGCAGGTGCTTGAACATCACTCAGCGCT
CTGGATCCAAGAACAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAATCTTTAACTCACTAGCTAG
CGGCGGCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC
TGACCAAGACAGCCCCCTTGAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT
TCTTGGGCAACCATATGTGGAGACCAAGGGTCAGTCTCTGGCAGAACAGATGCCACGAGTATCAAGGCAGG
AAAGGGTGCCCTCTTGGGTAGCAGGAGTCAGGGGCTGTACCTGGGGGTGCCAGGAAATGCTCTTGACCTAT
CAATAAAGGAAAAGCAGTAAAAAAGGAAAAAAGGAAAAA

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVDLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPTGPNLTHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESS
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQSRSLNYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTT
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQQPKRPQKHQKADIHLVPVLRGQAGEPCEVGQSHKVDVKEAMMEA
GWDPCLOAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEPGGS
RSAIPDTDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAASGMKVQGDPPGKGTGTEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCTTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTGAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAAATGAACCTGTGTGTAATCTGCTGATCCTGGTTTTCATGGTGCCTTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTCTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAGTGAAGTCTC
ATGGCTCTTCTTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGAATGATAAAAAGTGTACCCTTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTGACAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT
TCCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCCTCCAATGTCATTGTCCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAAGTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTAAGGTTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAGGGCGGCGGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTGTTTATTGCAGCTTATAATG

FIGURE 172

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS
SKSSNVIVLLLAQIMGMVFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 173

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNANACTATTTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

FOOTNOTES

FIGURE 175

GTGTTGCCCTTG GGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTC

FOOTNOTES

FIGURE 176

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGATTTGCTACCTTTT
TGGCTCCCTGCTCGTCTGAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGGCGAA
GGAGGGCGAGCCAGGCAGCCTCTTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATCGCACTGGAGGCCCTTTCGCTTG
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
GGAGAACCAGTGGTTGGGAGTCACTGTTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACAGATCCTGGAGACGCGGGATATGATTGGTTCGCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGCGACAGCTGCCGCTTCTCCCTGATAGCCACTACCTCCTCTTGGGGCCCCAGGAAC
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG
TCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCA
CAAGGGTGTCTGGTTCATCCTGCGCAAGGACAGCGCCAGTCCGCTGGTGCCTGAGGTTATGCTGTCTGGGAGCG
CCTGACCTCCGGCTTTGGCTACTCAGTGGCTGTGGCTGACCTCAACAGTGTGGTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTCTGTGTATGTGTACTTGAACAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTTCGGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAAGATGGCTTTCCAGATATTGAGTGGGTGCCCTTTGATGGTGTGGGAAAGTCTTTCATCTACCA
TGGGAGCAGCCTGGGGGTGTGCGCAAACCTTACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTGAGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGTCTTTCAGGGCCAGACCCATCCTCCATGTCTCCCTGAGGTCTCTATTGCTCCACGAAGCATCGACCT
GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT
TCCCCGTGTGACCTTCTGAGCCGTAACCTGGAAGAACCACAGCACCAGGCTCCGGGCACCGTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGT
AGTGACCTTGTCTTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCCTCAGTGGC
CCCCATCCTCAATGCCACCAGCCAGCCAGCACCAGCGGGGAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACC
TCTGCCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTGTGGGAGCCAGTCAATTGGCCTGGAGCTGAT
GGTCACCAACCTGCCATCGGACCCAGCCAGCCAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGTCGGGGCCCTGGACCTGCGGAGAAGCCACTCTGCTGTCCAA
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCATGAAGAGAGGTGCCAGGTCACCTTCTACCTCAT
CCTTAGCACCTCCGGGATCAGCATTGAGACACGGAATGAGAGTAGAGTCTGTGTTGGCCAGCATCAGTGAGCA
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTCTGGTGTGGTGGAGGGGCGAGAGGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT
CAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTCCGCTCAGAACCCCTGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGCGCGCGGA
GCTGGAGCCACTGAGCAGCAGGAGCCTGGTGGCGGAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGTC
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGACGGCCAACTGTGTGGTGTTCAGCTGCCCACTCTA
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAGTGTGTTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA
TGCCTCCACAGTGTATCCAGTGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCTGGTGGG
CATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTT
CAAACGGGCGAAGCACCCGAGGCCACCGTCCCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCCGCGGGAGGGCCCGGATGCACA
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCC
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCATCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGCTGGTGTGCATCAAGATTGGCAGGATCGGCTTCTCAGGGGCAAGACCTTCCCACCCACAAGAAC
TCCTCCCACCCAACTTCCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGTCTGTGCAAGGTGGGGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT
GTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCCTTAACCTAGAGGGTGGGGAGGAGGTTGTGTCACTGA
CTCAGGCTGTCTTCTTAGTTTCCCCTCTCATCTGACCTTAGTTTGTGCCATCAGTCTAGTGGTTTCGTGGT
TTCGTCTATTTATTAATAAATATTTGAGAACAATAAAAAAAAAAAAAAAAAAAAA

FOHET-1304E00T

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFCG
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVVYVLYNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDNLNQGDFPDIAVGAPFDGDGKVFIYHGSSLGVVAKPSQVLE
GEAVGIKSFYSLSGSLDMMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCF SYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQ PSTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN
ENASHVECELGNPMKRG AQVT FYLILSTSGIS IETTELEVELLLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVYEVT VSNQGQSLRTLGS AFLNIM
WPHEIANGKWL LYPMQVELEGGQGPQKGLCS PRPNILHLDVDSRDRRRRELEPPEQQEPGE
RQEPSMSWWPVSSAEKKKNITLDCARGTANC VVFSCPLYSDRAAVLHVWGRLWNSTFLEEY
SAVKSL EIVRANITVKSSIKNLMRLDASTVIPVMVYLDPM AVVAEGVPWWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGS PRREGP
DAHPILAADGHPELGPDPGHPGPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 177

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAACAAGATGCTCAAGGTGTGAGCCGTACTGTGTGTGTGTGTCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAGGCCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTGCATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTGGACAGTGCTGGTGTGTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTACAGAGAACAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPI
CKDSLGMWFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDEGGYKPTQCHGSGVQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 179

FIGURE 180

CAGACTCCAGATTTCCTCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC
GCTCTGCCTCCGGTGCTGCTGCCTGGGGCGCCGGCTTACACCTTCCCTCGATAGCGACTTCACCTTTACCCCTT
CCCCCGGCCAGAAGGAGTGCTTCTACCAGCCCATTGCCCTGAAGGCCTCGTGAGATCGAGTACCAAGTTTTA
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAAGGCAAACTTAGTTTGTGAACAAAGAAAA
TCAGATGGAGTTTCACTGTAGAGACTGAAGTTGGTGATTATGCTTGTCTGTGCAATACATTACGACCATT
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG
AAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC
AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCAATGGTGGTGGTGTCAGCCATTCAAGTTTTAT
ATGCTGAAGAGCTGTTTGAAGATAAGAGGAAAGTAGAATTA~~AA~~AACTCCAACTAGAGTACGTAACTATGAAA
AATGAGGCATAAAAAATGCAATAAACTGTTACAGTCAAGACCATTAATGGTCTTCTCCAAAATATTTTGATATATA
AAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG
TTGTACTTAAGTGTGTAACAGGAATATTTTGAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT
TTTCTAACTTTGAAAAATTTTGCAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC
AGTCTGTTTTTAAACAGGTTCTATTACCAGAACTTTTTTTGTAATTCGGGAGTTACAAATTAATCTGTGGAAGTTT
TCAGTTTTAAGTTATAAATCACTTGAGAATTACCTAATGATGGAATTGAATAAATCTTTAGACTACAAAGCCCAA
CTTTTCTCTATTTACATATGCATCTCTCCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG
AGATTTTTATAACCAAATACATTTTCAGTGTAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
CCAAAAGCTGACATTTTCACGATCTTAAAAACACAAAGTTACACTTACTAAATTAGGACATGTTTCTCTTTG
AAATGAAGAATATAGTTTAAAAGCTTCTCTCCTCATAGGGACACATTTTCTCTAACCCTTAACTAAAAGTGTAGGA
TTTTAAATTAATTTGAGGTAAAATAAGTTTATTTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
TAATCATGTTATGTTAATTTTAAACATGATTGCTGACTTGGATAATTCAATTATTACCAGCAGTTATGAAGGAAATA
TTGCTAAAATGATCTGGGCCTACCATAAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAAACAGGAA
AGAAATTTAGAAAACTTGAGAAAACTTAATCCAAAATAAAATTCACTTAAGTAGAACTATAAATAAATATCTAGA
ATCTGACTGGCTCATCATGACATCTTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
AACTTTGGCTGTAGGTTTATTTTCTACAAGAATTTCTGGTTTGAATTTATTTTGTGAAGCAGGTACATTTTATA
AAATGTAAGCCCTACTGTAAGGTTTACAGCTGGGTGTACATATTTATTAATAAATTTTTATTATAACAACTTTTAT
TAAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTTAA
CCTTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGTCTTAC
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAATTTTAAAGTTATGCCCACTTTATAACGTTGTTTTAT
GACTACATGTTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT
CTGATGAGCAATAATGATAACCGAGAGTGATTTTCACTTACATCATGATAGTATAGAAAGAGATACATTTCCC
TCTTAGGCCCTGGGAGAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAATGCCGTAT
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA
AGGTCAATAAGATCCTTGCCATAGATACCCCTCCCTTTTGGCTGTTAAATTTGCAATGAGAAGCAAATTTACA
GTACCATAACTAATAAGACGGGTACAGATAAACTACTGCATCTTTTCTATAAACTGTGATTAAAGAAATCTTA
CTCTCTGTATGCTGTTACTGTACTGTACTCTGTACTCTTCACTTCACTTCAATGAATTTGTTACATAATCTCT
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTTCACTAGTAACTTCTTACCATATAAAAAAGATAATTGCTT
TATTTGAAAAGAAATTTAGGAATACTAAGGACAATTTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
CATAACCAAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTAAATATTTCTAAAGACATACTGTTTATCTGCTT
CATATGCTTTTTTAAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATGAGTAAAGCTGTTTATCACTT
AACAGCTCATTTTGTCTTTTTCAATATACAAAATTTAAAAATACTACAATTTTAACTAAGGCCCAACCGGATTTT
CATAATGTAGCAGTTACCGTGTTCACCTCAACATAAGGCTTAGAGTTTGCTGTGATATGCATTTGGATGATTAAT
GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGGTGTGTTGTAATTTTATGGTAAAATTAATCCTTCTTA
CACATAATGGTGTCTTAAATTTGACAAAAAATGAGCACTTACAATTTGATGTCTCCTCAAATGAAGATCTTTTAT
GTGAAATTTTAAAGACATTGATTCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAAATCAGTGTG
CTCAAACCTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA
AAATATCAAGAGAAAA

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLFPFVLLLAALPPVLLPGAAGFTPSLSDFTFTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFTEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

FOOTNOTES: 18024001

FIGURE 182

CCATCCCTGAGATCTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCC
TTCTTTTTCCTTTTCTTCACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

40201-130100

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM

DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS

TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPHYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

FOOTNOTES

FIGURE 184

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCGTGTCTGTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGGCCCTCACGCTC
CTCCCCTCTTGAGCCTCCGACTGTAGAGTCCCCGCCCCACCCCATGGCCCTATGCGGCCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAA

FIGURE 184

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FQGDSTVTKSCASKCKPSDVDGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

FIGURE 185

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTTAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTTCTTTATGGAACCTCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

Footnote: HBB, FOOT

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

FOOT-HEAD-FOOT

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCTCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

FOOTNOTES

FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCGCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG
 CTGGGCCGTGCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA
 GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA
 AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCT
 TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
 TTAAATCAGAACTTGCATAAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
 GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG
 AGTGTCCAAAACGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA
 AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
 TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
 CTATTATCGTTATGATTTTTGGTATTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC
 TGCTGTTAATTTCTGAGAACTGTGGTTTGTAAATTTTTACTCCCCAGGCTGTTTCACTGCCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGTATAGAAAT
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCCAGTGAATA
 TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG
 GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGTCTGCTGGTATTGGCTGGCTGATCACTTTTTGTTCAAA
 AGGAGGAGATTGTTTGACTTTCAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA
 AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAGTACTTTCCGCAACACACTAGAGGATCGTTT
 GGCTCATCATCGGTGGCTGTTATTTTTTCAATTTTGGAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAAT
 AAAAATCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTCTCTGACCCAGACATCTGTAGTAA
 TCTGTATGTTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA
 GAAGATTCTATATGATATACTTGCCCTTTGCCAAAGAAAGTGTGAATTCATGTTACCACGCTTGGACCTCAAAA
 TTTTCTGCCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACT
 ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAAGTTAAGTTTGTACACTAGATTTGTACAGTTTATGA
 GGGACTCTGTACATGTATAACATTCAAGCTTATCCAACACAGTGGTATTCAACCAGTCCAACATTATCAGTGA
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTTATAGAGGATCTTATGAATCCTTCAAGTCTCCCTTAC
 ACCCACCACCTTCAACGAAGTATTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG
 GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAAGTGGCCCGGACATTAAGTGGACTGATCAACGTGGG
 CAGTATAGATTGCCAACAGTATCATTTCTTTTGTGCCAGGAAAACGTTCAAAGATACCTGAGATAAGATTTTTT
 TCCCCCAAATCAAATAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATCCCTGAGAAT
 CTGGGGCTAGGATTTTTTACCTCAAGTATCCACAGATTAACACCTCAGACTTTTCAAGTAAAAAGTTCTACAAGG
 GAAAAATCATTGGGTGATTGATTTCTATGCTCTCTTGGTGGACCTTGCCAGAATTTTGTCTCAGAAATTTGAGCT
 CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGCCTATCCAAGTGTAAAGTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATTGGAACTCTCCGAAATCAAGGCAA
 GAGGAATAAGGATGAACTTTGAATAATGTTGAAGATGAAGAAAAAGTTTAAAAAGAAATCTGACAGATGACATCAG
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGACGTTGTACTGCCA
 GAATTATCTACAGCACTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA
 GACTTTGCAGGCTATAATATATGTTTACACATGAGAACAAAGATAGAGTCATCATGTATTCTTTGTTATTTGCT
 TTTAACAACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCACTCCATG
 GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAAGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCAAGTTTTTTGGCTGACCTGAAAAGAGGTAAT
 TAGTTTTTGGTCACTTGTCTCTTAAATATGCTATCCCTAACCATATATTTATATTTCTGTTTAAAAACACCCAT
 GATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCTCTCA
 AAGGTTGAAAAATGCTTTTAAATTTTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
 AAATTTGAGCAACAGTAAGTGACAAATTCTGTAGTTTGTCTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA
 TAGCAATTAAGTGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA
 TGTGTTTCAATGATTTTCTGAAATTTGCTTTTATAGAAATTTTCCACTGATAGTTGATTTTTGAGGCATCTAATAT
 TTACATATTTGCTTTCTGAACCTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTTTCTTTTATAGTTTGG
 TTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAATTACTTTACAGGTTGTTTTACTGTAGCTTAT
 AATGATAGTGTAGTTATTCCAGTTACTAGTTTACTGTGAGAGGGCTGCCTTTTTTCAAGATAAATATTGACATAATA
 ACTGAAGTTATTTTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGATCTTCTAGTTTCTGTGTTGTTTGA
 CTCAAAGAATCAAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGTAAAAAT
 CCAATCAGTCAAAGAGGTCAATGAATTAAGGCTTGCAACTTTTTTCAAAAAAAAAAAAAAAAAA

FIGURE 189

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLDNQGGQYESWNYRYDFGI
YDDDPEIITLERREFDAAVNSGELWVFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP
SLAVFKGQGTYKEYEIIHHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS
AEQILEFIEDLMNPSVVSILTPTTFNELVTQRKHNEVVMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGG
GTCGTTGGTGAAGTTTTTCATTCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTACCA
AAAATCCAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTCTGAG
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCAATCAATGCTGCAAAGCTTTATTTACATTTTTT
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCTT
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTCAGCATTGAAAGATTTCCCTAGCCTCTTCCTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCTCTATATTTCCCTCCCTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

FIGURE 191

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESIVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAAECKRLGVTAHAYVVDSCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFGHRLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSRID
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

10047094-10404

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCGCCGGGGC
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTTCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCT
CTAGGCCGCACACGGGGCCGCCGCTGCCCACGCCCCGGGCCGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCGACGCCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGACACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCCGTGCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCCGAAAACCTCCTCC
GAGACTGAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTA
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESSVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLHHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELNEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLEDAQAQLQLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FOOTNOTES

FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCGCATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCTTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGTGCAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCGTGACGCCCCGATATCCCTTCCTGATTTCTCTCATTT
CTACTTGGGGCCCCCTTCCCTAGGACTCTCCCACCCAAACTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

FIGURE 195

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAFVNNGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLLDCVVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAVFLASEANFCTGIELLVTTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

TOH20T-1804T00T

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAAATGACTGGCCTCACAACTG
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTAGCCAGGTTCTGTGCGCCGCCG
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGTAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKQGGRPGPLAPGPHQVPLDLVSRMKPYARMEEY

ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL

GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

FIGURE 198

FIGURE 199

CGCCGCCGACGCGCTAGCGCGGGTGGCCCTTGCGTCTCCCGCTTCTCTTGAAACACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCCGGAGAAGCCTCGCTCG
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCGGAGGAGCGCGCTGCCGCCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTAGAATGGGAGGCTTTTTGCAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTTGAGTG
GCCGCTTCTTTGTCACTACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAATT
CCTGCTTGGTGTTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTTGGCCTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGTTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAGTCAGCATGCTGACAAGGGAC
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAACAATATGTGAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAATCCTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCAGGTGT
GACAATCAGGATATAGAAAAACAAACGTAGTGTTGGGATCTGTTTGGGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGAGGAGGCCATTCAGTCCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATTCAGGAAACATCAGGCACCACAGTGATGAAAAATCTTTCACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTACGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATTTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAATAACTAAAAAACCTTCTGATTTTCTTTCAGTGATGTGCTTTTGGTGAA
GAATTAATGAACCTCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC
TTCCAAAGAATTATATCTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPSCQQTDSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISECFYVPLPRHLSEQRSEQNRRSEEAHRAEQLODAEEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

10017084-102401

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGGAATATCATCCTGATTTAGAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATTACAGTGTCACTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG
TTTAGAGAGCTTGGCCAACCTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTGCGACCTACAGGTAGGCTAGTATTTATTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTTATTTTGGAGATAGGGTCT
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAACGG
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCCTCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACCTCTGACCTCAAGTGATCTGC
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
TGATAAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTCAGTAATTACTGTAAATGGTATTATTGGAATGAACTATATTTCTCATG
TGCTGATTTGTCTTATTTTTTTCATACTTCCCACTGGTGCTATTTTTATTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTTATGTTATGTGGATTTTCAT
TTCAATAAAAAAACTCTTATCAAAAAA

104201-1504-001

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGS CAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSPPCPNWIIEKSCYLFMSLSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

TOP SECRET FOOT

[illegible]

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFCSSQRNQTHRSSLHYKPTPDLRISIENSE
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWSPQNISLPSAASFTHSFHSPHTAAHNASVDMCELKRDQLL
SQFLKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTLQFQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTPVVLTFQHQQLQPKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSFCFNHLYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSAALCLVTIAAYLCSRVPVLP
RRKPRDYTIKVHNNLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGLIFIWYSMRLQARGGPSPLKSNDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 204

[illegible][illegible]

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA
TCCTTTTCAAAACTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCCT
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAGAGAC
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCGGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGC
TTCTCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTC
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
GAAGTATTCACAGCCCAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTTACGTTTGTATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTCTCTGGTACTGTACCAG
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTCTTCTGAACCAGGGT
TCTGCATCCACTACAACATTGTCTATGCCACAATTACAGAAAGCTGTGAGTCTTCTAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT
CAGTGTCCATAAGGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGTTAAACGCTGTG
GTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAAGCTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCACTTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
ACAGCTCTTTTGGAGAGGAGGCTTAAAGGACAGGAGAAAAGGCTTCAATCGTGGAAAGAAAATTAAATGTTGTAT
TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTT
GATACGGCTTAGGGTAATGTGATACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC
TCTAAAGCTCCATGTCTGGGCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTATATTCACAT
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTAACCTGT
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAATAATTTCTGCCATTTAGAAGAAGAGAACTACA
TTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG
TTTCATTGTGTACATTTTTATATTTCTCTTTTACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT
ATTTTTACCAAAGGTATTTAATATTTCTTTTTATGACAACCTAGATCAACTATTTTTAGCTTGGTAAATTTTTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA
GACTTTTTGAAAATAATTAATTTATCATATCTTCCATTCTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA
AAGTAGACATTGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTGAAGAAAGACTTGGCAGCTTCTGATAAAGCGTGTGTGCTGTGCAAGTAGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA
GAAGTATGCTCTTAACCAGTTCATTATTGTACTCTGGCAATTTAAAGAAAATCAGTAAATATTTTGCTTGT
AAAATGCTTAATATNGTGCCTAGGTTATGTTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAATAAAGA
ATGTGGCTATTTTGGGGAGAAAATTAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGTAATGCGGCC

104207-1302-001

FIGURE 207

MSLFGLLLLTSAAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPKGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKSRVVDLNLLEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSGTGG

Signal sequence:

amino acids 1-14

104207-180200

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTTCAACCAGACCTCTACATTCCATTTTGGGAAGA
 AGACTAAAAATGGTGTTCCTAATGTGGACTGAAGAGACAAATTCTTATCCTTTTAAACATAATCCTAATTTCC
 AAACCTCTTGGGGCTAGATGGTTTCTTAACTCTGCCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
 ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTTCCACGAACACCACGAACCTCACCCCTC
 ACCATTAAACCACATACCAGACATCTCCCGAGCGTCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA
 TGCAACTGTGTACCTATTCCACTGGGGTCAAAAACAAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGGAAGC
 TTTAGTGGACTCACTTATTTAAAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCCG
 CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACAAACATCTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
 AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTTATCGAAATCCTTGTATGTTTCATATTCAATAGAGAAA
 GATGCCCTTCTTAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGCTCCCTACTGTT
 TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC
 CTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTTGCCCTCGTTGTATAATGCCCATTTCTTGTGCGCCG
 TGTAAAAATAATTTCCCTACAGATCCCTGTAATGCTTTTGATGCGCTGACAGAAATTAAGTTTTACGTCTA
 CACAGTAATCTCTTCAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAATGGATCTGTCC
 CAAAACCTTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTTCTCCCGAGCTCATCAATTGGATCTG
 TCTTTCAATTTTGAACCTTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG
 AAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTGCCATTACATAATCTTCAA
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAGA
 CTGAAAGTCATAGATCTTTCACTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT
 GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTTGGAAACAATTACATTATTTTCAATATGATAGTATGCA
 AGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTTATGTCTGTTAATGAAAGCTGTACAAGTATGGGCAGACC
 TTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGTCTCTGATTTTCAGCATCTTCTTTCTCAAATGCCTG
 AATCTGTCAAGAAATCTCATTAGCCAAACTCTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTG
 GACTTCTCAAACAACCGGCTTGATTTACTCCATTCAACAGCATTGGAAGAGCTTCAAAAACCTGGAAGTTCTGGAT
 ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT
 CTGCAGAACTGATGATGAACGACAATGACATCTTCTTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG
 AATCTGCTAAATTAGAGGAATTAGACATCTTAAAAATTCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGT
 ATGCCTCCAAATCTAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT
 CTAAAGAACCTGGAAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAACCTGTTCC
 AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC
 CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAGACCAGCTTCCAGAAAATGTCCTC
 AACAATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG
 GTTAACCATACGGAGGTGACTATTCTTACCTGCCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
 CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
 TCTGTATCTCTTTCTCATGGTGATGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT
 TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT
 GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAAACTGGAAGACCCCAAGAGAGAAA
 CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA
 CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAAGATAGCATTTTAC
 TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAG
 TCCAAGTTCTCAGCTCCGAAAAGGCTCTGTGGGAGTTCTGTCTTGAAGTGGCCAAACAAACCCGCAAGCTCAC
 CCATACTTCTGGCAGTGTCTAAGAAGCGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA
 ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

[illegible]

Signal sequence:

Transmembrane domain:

amino acids 840-860

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQNDSVIAECSNRRLOQVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSQLQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPPCVPCDGGASINIDRFAFQNLTLQRLYNLSSTSLRKINAAWFKNM
PHLKVLDLEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNLEIIYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFFEDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDEV
LDLSYNHYFRIAGVTHHLEFIQNFNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDLS
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID
NMQSINQSKKTVFVLTCKKYAKSWNFKTAFYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGFLWQTLRNVVLTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 211

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTG
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCCAGCGCCCCAGGCTG
GACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTCCTCCTCCCC
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCCGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTGA
AAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTGTATTATTGCAGCTTATAATGGTTACAAAT

10017084-102401

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSDGTLCPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FOOT-130400T

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGGCCGGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTGC
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTCCTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTCCTTCCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAATAAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLADGTLCPVKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

1041207-13047007

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC
TTCCAGCAGCTCGGCCGCA¹TCGACTCCCTGAGCGAGCAGATTTCTTCTGAGGAGCAGCT
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCTCCTCCCCTTCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLASADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FOOT-180XFOOT

FIGURE 218

GGTTGCCACAGCTGGTTTATGGGCCCCGACCACTGGGGCCCCCTTGTCTCAGGAGGAGACAGCCTCCCGGCCCGGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCCTGCCGTACAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGTGGGCGGTTTATCGGGAGG
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTCTCTCGTGAATCGCAAAACCCATTTTGAGAGCAGGAATTCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAATGGGAGAACTCCCAGGCAGGAACACCTTTTGCTGTG
ATGGCCGCGTCATGATGGCCCGGCAAAAGGGCATTTTCTACCTGACCCCTTTTCTCATCCTGGGGACATGTACAC
TCTTCTTCGCTTTGAGTGCCGCTACCTGGCTGTTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGCGCTACCAGATG
AAGCAGCTTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCCTCGTA
TCAAGAATTTCCAGATAAACAACAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGCTCCCC
GGGCCTCCCATTCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTG
TTGGAAGAGGAACTACCGCTACTTCTACCTTTCATCCTTTCTCTCCCTCCTCAATCTATGTCTTCGCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGAGACATTGAAAGAACTCCTGGAAGT
TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTGCGTGGGACTGACTGGATTTTCTACTTTCTCGTGG
CTCTCAACAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCCGCTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCTTGCCCCCAGTGCTGGATCGAAGGGGTA
TTTTGCCACTGGAGGAAAGTGAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTT
TAATTAGGGCTATGAGAGATTTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACT
CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGTCCCCCTTGACCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCAC
TGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTAGGAATGGGACAGGTACCT
TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTGAAGTCTGCTCCCATTAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACCTTGGTCATTTCTTTTCTCAGAGGAAGCCCCGAGTGCTCACTTAAAC
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAATGCTAACCAAGTCTTCCATTAAGCCT
CGCTGAGTGAGGAAAGCCGACACTGTGCCCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT
ATGGTAACCACTGGGGCTTCTCCAGCCCCGCTCTTCCAGCACTTCCACGGCAGAGTCCAGAGCCACTT
CACCTGGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT
ATTATATGTGGCTATATTTCTAGAGCCTGTGTTTTCTCTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGGAGTGTAACCGGAACTTTTCATCTATTTGAAGGCGATTAACTGTGTCTAATGCA

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPCWVGNCVGKRNRYFYFYL
FILSLSLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLCFFTLWSVVGLTGFHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPQEAAEA EK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

total: 150200

FIGURE 220

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

TOH20T H304FOOT

FIGURE 221

GTTGTGTCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAGAGTTTTAAAAAGAAATTGAA
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

FIGURE 221

FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGTLOCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHNTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKF

Signal peptide:

amino acids 1-28

FOOT - FOOT

FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

FIGURE 223

FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCCGACTCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCACAGCACCTGCCTTACA
GAGGCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGCTGGATTGCGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCTACAGGTGGAGCGCATTTGAGGAGCTGGGAGCCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACCACTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATAAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTGAGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
CTGTCTTTCTTGTGTCACCATTTGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACTAAGAATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCAACCCCAAGGCCCTGAACCTTCGGTGGCATC
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGGAGTATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACACGGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAAACATTACTGACAACGGGGGGCTGAAG
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGG
CACTTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCTGACAAAGCTGTTTGCTCTTGGGTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCAATTG
TGCTCTGCTTTGGGGGTGCCCCTGCCTCCAGCAGAGCCCCACCAATTCACTGTGACATCTTCCGTGTCAACCT
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

FIGURE 224

FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP SH
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFT VYISADSKSSNSNVIQVDQSGLFLPSRDYYLNRTANEKVL TAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLL ETLYGTTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTA FEELGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQT VNAYYLPTKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLA AFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNP GQLCEVW

Type II Transmembrane domain:

amino acids 32-57

FIGURE 226

CCCCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCGCTCCCGCGCCCTCCTCCCTCCCTCCCTCCC
CAGCTGTCCCGTTCCGCTCATGCCGAGCCTCCCGCCCCCGCGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCT
CGGCTCCCGGCGGCGCGCGCGCGCCAGAGCCCCCGTGTGCTGCCATCCGTTCTGAGAAGGAGCCGCTGCC
CGTTCCGGGAGCGGCAGGTAGGTGGGCGCCCGGGGAGGCGCGGGCGGGGAGTCCGGCTCGGGGCGAGTCAGCGC
CAGCCCCGAGGGGGCGCGGGGCGCAGGTGGCTCGGCGCGCGGGCGCCCGAGGGTGGGCGGGGGCAGAAGGGC
GCGGTGCTGGGACCCGGGACCCCGGGGACCCCCGGGGCGGCACACGGCGGAGCTGGGCGAGCGGCCCTCAGC
CAAGCCCGTCCCCGAGGCTGCACCTTCGGCGGGAAGGTCTATGCTTGGACGAGACGTGGCACCCGGACCTAGG
GGAGCCATTCCGGGTGATGCGCTGCGTGTGTCGCGCTGCGAGGCGCAGTGGGGTCCCGTACCAGGGGCCCTGG
CAGGGTCAGCTGCAAGAACATCAAACAGAGTGCCCAACCCCGGCTGTGGGCGAGCCGCGCAGCTGCCGGGACA
CTGCTGCCAGACCTGCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTGCGAGGCGGTGGCACAGCCCCG
AGTCTGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACCGCCCTACCAGGATCCGCTT
CTCAGACTCCAATGGCAGTGTCTGTGTTGAGCACCTTGACGCCCCACCCAAGATGGCCTGGTCTGTGGGGTGTG
GCGGGCAGTGCCCTCGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCA
CCCTTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGTCCCAGAGACCTTCAGTGCCATCCTGTGCA
TCTAGAAGGCCCCACCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA
TTTTTTGCTGCTCTTCCGAGGCTTGCAGGACTAACCCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCA
GCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAACAGGCTTTGCTGAGGTGCTGCCAACCTGACAGT
CCAGGAGATGGACTGGCTGGTGTGGGGAGCTGCAGATGGCCCTGGAGTGGGCGAGGCGAGGCGAGGCTGCGCAT
CAGTGGACACATTGCTGCCAGGAAGAGCTGCGAGCTCTGCAAGTGTCTTTGTGGGGCTAATGCCCTGATCCC
AGTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCTGATCCTCCAGGTGCAATT
GGTAGGGACAACAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTCAGCGGAGGGATCAGCCCACTGTCTT
GTGCCACATGGCTGGCTTATCCTCCCTGCCCGCAGGCGTGGGTATCTGCCCTGGGCTGGGGTCCCCAGGGGGC
TCATATGCTGCTGCAGAAATGAGCTCTTCTGAACGTGGGCACCAAGGACTTCCAGACGGAGAGCTTCCGGGGCA
ACGTGGCTGCCCTGCTGCTGAGGAGTAGCGCCCGCCCTGCCCGTGGCCCTAGCAGGAGCCCTGGTGCTACC
CCCTGTGAAGAGCCAAAGCAGCAGGGCACGCTGGCTTTCCTTGGATACCCACTGTCACTGCACTATGAAGTGT
GCTGGCTGGGCTTGGTGGCTCAGAACAAAGGCACTGTCACTGCCACCTCCTTGGGCTCCTGGAACGCCAGGGCC
TCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAGGCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACGTCTGCG
GCACCTGGCAAAGGCATGGCTTCCCTGATGATCACCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCT
CTCCTCCCAGGTGCATAGCCAACCAATGTGAGGTGGCGGACTGCGCCTGGAGGCGGCGGGGCGGAGGGGGT
GCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGC
CAAACCTGGTGGTCTGGGCGGCCCCGAGACCCCAACATGCTTCTTCGAGGGGCGAGCGCCCGCCAGGGGCG
TCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGT
GGTGTGCCACCCGCGCAGCTGCCACACCCGGTGCAGGCTCCCGACCAAGTGTGCCCTGTTTGGCTGGCTGCTA
TTTTGATGGTGACCGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCTTTGGCTTAATTAA
GTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCACTGTCCCCGGCTGGC
CTGTGCCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAAACAGTGTCCAGGTGAGGCGCCACCCGCTGGG
GGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGTGCGGAGTGGTTCCAGAGAGTCAAGAGCTGGCA
CCCTCAGTGCCCCGTTTGGAGAGATGAGCTGTATCACTGCGAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT
GTGAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCAGGGAGGTCCCTGAAGAAGCTGAAGGTCA
CTGTGCTCCAGTGCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTGTACAGGCGAGGGGTGCCTCACTGTGAGC
GGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTGCATGCTGTTCCCGCTGCACGGCCCCACC
GGCGGCGTAAGTGAGGGAGTCCAGGGTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAG
GGAAGGGAGCACTCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCCTCACAGCA
ACCTGGTGGAAATGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGAAATTAAGCAACGAG
ATGAAGGTCAACCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGCCTTTCTGGGACCAAGGCAGGGATGCTT
TGCCCTGCCCTCTATGCCCTCTCTGTGCTCTCACTCCCTCTCCCTCTCCAACATTCCCTCCCTTCTGTCTCC
AGCAGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAACCGAAGGCTCTTAGGGAGCAGCCAGAGGGCC
AAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCACTTCTCTGTGGGAAG
CCCAGTGCCTTGTCTCTCTGTCTGCTCTACTCCACCCCACTACCTTGGGAACCAAGCTCCACAAGGGG
GAGAGGCGAGTGGGCCAGACCGAGGTCAAGCCACTCCAAGTCTGCCCTGCCACCTCGGCCTCTGTCTCTGGAA
GCCCCACCCCTTCTCTCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTTATCTTCACTCAGCACCAG
GGCCCCGACACTCCACTCCTGTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTGTATTTATTAAGAA
ATTTCTTTTTCAGTCTTTGGGCATGAGGTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCTGGTGGAGAAGGG
GCNAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGACCTGGAGAGGCAGAGGATAG
CGTGGCCTTTGGCTGGCATNCCTGGGTTCCGCGAGAGGGGCTGGGGATGTTCTTGAGATGGTCTAGAGACTCAAG
AATTTAGGGAAGTAGAAGCAGGATTTTGAAGTCAAGTTTAGTTTCCACATCGCTGGCCTGTTTGTGACTTTCATG
TTTGAAGTTGCTCCAGAGAGAGAAATCAAAGGTGTACCAGCCCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTCT
TTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT

FIGURE 226

FIGURE 227

GGCCGAGCGGGGGTGTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC
TCCACCATGAACGTGCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGGA
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCCCT
CCTTTCTTTCTTCTTTTCTTCTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCCCTTCCCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCTG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCTTGAGGATTTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

FIGURE 227

[illegible]

ATGCCCTACTACCTTCCAACCTAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTCTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCCCT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGA CT CAGCTCTGTC
TGGCTCACCTCAGGGCTACCCCCACCTCACCCTGTGCTCCTTGTGCCACTGCTCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

FIGURE 230

MMLLVQGACCSNQWLA AVL LSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED
GASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKR DYSLQIQNV DVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIYDISNDMTVN EGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFPDVRKV KVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL
NPPSTAQYGITGSADVLFSCWYLVLT LSSFTSIFYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTACCAAATTGCAATGGAGCCTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTCTGAATCTGCAGGC
GCGGCTCCGGGTCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT
AGACAACTTCACTCAGAACCCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCAACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCGGGACCACCTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAGGGTGCTCCAGGGAAGCAAG
GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT
GGCCCCAAAAGGGGAAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGAGGGCCTCCTGGAGCCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCCACAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCGCGGCCCTCCTGGTGCAGTGGGACACCCAGGTGC
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCAGGCCCCGAGGTGTGAAGGGAGAACAGGGGAGCCCAGG
GCTGGCAGGTCCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTGCGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTTCAAGTGTGCGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAAATAGCTGGGGCCATCA
TGAATGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGACCCCGAAACCCCTTTCA
CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVNFTQNPFGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPPAEKGAAGAMGRD
GATGPSGPQGPVGKGEAGLQGPQGAPGKQATGTPGPQGEKSGKDGGLIGPKGETGTKGE
KGDLLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPGAKGDQGPGLQGVPG
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKSGKDTGLQGQQGRKGESGVPGPA
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDDNVQCRGTESTLW
SCTKNSWGHHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

FIGURE 232

FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGGAGAACACCATTCTGATTTT
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

FIGURE 233

FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

FOOT-430-0000

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCCAGCCTGCAGGG
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC
 GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATG
 TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCGCTGGCTGTG
 CGCTGGGGCGCTGGTGCTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCGGGTGGTTTA
 TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC
 AGGAACAGAACAAAACCTTTCAGCTTGCAAAGCAAATTCAATCCAGTGGAAGAATTGGCC
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCCTACCCAAATAAGACTCATCCC
 AACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTCAACACATCATTATTTGAACC
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTCTCTCCTC
 AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAA
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT
 TTTAGAGGAAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT
 CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCT
 GGAGGTGGTGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACC
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAA
 GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC
 TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
 CTTTACTGGAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATT
 CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT
 TGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA
 CAATTTTGTGTTGCAAGCTGGGATGCAGAAAGATTTGGTCTTCTTGGTTCTACTGAGTGGGCA
 GAGGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
 AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG
 ACTAAAAAAGTCCTTCCCCAGAGTTTCAGTGGCATGCCCAGGATAAGCAAATTGGGATCTGG
 AAATGATTTTGAAGTGTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA
 AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT
 GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCG
 AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTGAGATTATG
 CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT
 TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA
 TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTATTTGATCCATTAGGGTTACCAGAC
 AGGCCTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC
 ATTCCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCTTCCAAGGCCT
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT
 TTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTATGTCA
 CTCAGAAAGAATCGTAATGGGTATATTGATAAAATTTTAAAATGGTATATTGAAATAAAGT
 TGAATATTATATATAA

F0420T-1302100T

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQQRGNILNLNGAGDPLTPGYPANAYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVMMHIHSTNEVTRIYNVIGTLRGAVEPDYV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLQLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYES
WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWTNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHKNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713